

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 28, 2006, 18:18:07 ; Search time 151 Seconds  
(without alignments)  
2713.727 Million cell updates/sec

Title: US-10-726-093-10

Perfect score: 758  
Sequence: 1 MENELFCGSLVHPQWVLSA.....SRGLTQSSASQAECPCCSA 146

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-O=/abs/ABSSWB spool/US10726093/runat\_28082006\_121140\_25742/app\_query.fasta\_1  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rm1 -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humand0.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss08 -USER=US10726093 @CGN 1.1 204 @runat\_28082006\_121140\_25742  
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/ina/H COMB.seq:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCVUS COMB.seq:\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq:\*
- 9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq:\*
- 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758	100.0	1265	3	US-09-020-956-173 Sequence 173, App
2	758	100.0	1265	3	US-09-030-607-173 Sequence 173, App
3	758	100.0	1265	3	US-09-439-313-173 Sequence 173, App
4	758	100.0	1265	3	US-09-352-616A-173 Sequence 173, App
5	758	100.0	1265	3	US-09-232-149A-173 Sequence 173, App
6	758	100.0	1265	3	US-09-159-812-173 Sequence 173, App
7	758	100.0	1265	3	US-09-636-215-173 Sequence 173, App
8	758	100.0	1265	3	US-09-685-166A-173 Sequence 173, App

9	758	100.0	1265	3	US-09-115-453-173 Sequence 173, App
10	758	100.0	1265	3	US-09-688-489-173 Sequence 173, App
11	758	100.0	1265	3	US-09-679-426-173 Sequence 173, App
12	758	100.0	1265	3	US-09-759-143-173 Sequence 173, App
13	758	100.0	1265	3	US-09-651-236-173 Sequence 173, App
14	758	100.0	1265	3	US-09-030-606-173 Sequence 173, App
15	758	100.0	1265	3	US-09-657-279-173 Sequence 173, App
16	758	100.0	1265	3	US-10-012-896-173 Sequence 173, App
17	758	100.0	1265	3	US-09-116-134-173 Sequence 173, App
18	758	100.0	1265	3	US-10-144-678A-173 Sequence 277, App
19	695	91.7	484	3	US-09-621-976-277 Sequence 1, Appl1
20	660	87.1	4740	5	US-09-936-271C-1 Sequence 174, App
21	640	84.4	1459	3	US-09-020-956-174 Sequence 174, App
22	640	84.4	1459	3	US-09-439-313-174 Sequence 174, App
23	640	84.4	1459	3	US-09-352-616A-174 Sequence 174, App
24	640	84.4	1459	3	US-09-233-149A-174 Sequence 174, App
25	640	84.4	1459	3	US-09-159-812-174 Sequence 174, App
26	640	84.4	1459	3	US-09-636-215-174 Sequence 174, App
27	640	84.4	1459	3	US-09-685-166A-174 Sequence 174, App
28	640	84.4	1459	3	US-09-115-453-174 Sequence 174, App
29	640	84.4	1459	3	US-09-688-489-174 Sequence 174, App
30	640	84.4	1459	3	US-09-679-426-174 Sequence 174, App
31	640	84.4	1459	3	US-09-759-143-174 Sequence 174, App
32	640	84.4	1459	3	US-09-651-236-174 Sequence 174, App
33	640	84.4	1459	3	US-09-030-606-174 Sequence 174, App
34	640	84.4	1459	3	US-09-657-279-174 Sequence 174, App
35	640	84.4	1459	3	US-10-012-896-174 Sequence 174, App
36	640	84.4	1459	3	US-10-144-678A-174 Sequence 174, App
37	640	84.4	1459	5	US-09-621-976-1662 Sequence 524, App
38	640	84.4	1459	3	US-09-439-313-524 Sequence 524, App
39	588	77.6	765	3	US-09-636-215-524 Sequence 524, App
40	588	77.6	765	3	US-09-685-166A-524 Sequence 524, App
41	588	77.6	765	3	US-09-679-426-524 Sequence 524, App
42	588	77.6	765	3	US-09-759-143-524 Sequence 524, App
43	588	77.6	765	3	US-09-651-236-524 Sequence 524, App
44	588	77.6	765	3	US-09-651-236-524 Sequence 524, App
45	588	77.6	765	3	US-09-651-236-524 Sequence 524, App

## ALIGNMENTS

RESULT 1  
US-09-020-956-173  
Sequence 173, Application US/09020956  
Patent No. 6261362  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillin, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS F  
NUMBER OF SEQUENCES: 178  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/020,956  
FILING DATE: 09-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 173:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-020-956-173

Alignment Scores:  
Pred. No.: 4,3e-79 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0

US-10-726-093-10 (1-146) x US-09-020-956-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAGAAAGCAATGTTCTGCTGGGCGTCTGTCATCCGACGTGGTCTCTCAGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40  
DB 100 GCACACTGTTTCCAGAACTCTACACATCCGGGCTGGCTGCAGACACTTTCAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGlnAlaSerLeuSerValArgHisProGlnTrpValAsn 60  
DB 160 CAAGAGCCAGGAGCGAGATGTGTGAGGCGAGCTCTCCGTACGGACCCAGAGTACAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnSer 80  
DB 220 AGACCTTCTGCTGCTAACGACCTCATGCTCATATGAGACCAATCCGTCTCCAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlnAsnSerCysLeu 100  
DB 280 GACACCATCCGAGCATGACATGCTTCGCAAGTCCCTACCGGGGAACTTTCCTCCTC 339  
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGlnLeuThrGlyValLysLeuProSerSer 120  
DB 340 GTTTCGTGGCTGGGCTGCTGCGGAACTGAGCTACGAGTGTGTCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlnCys 140  
DB 400 AGAAGGTCTCTGCTGACGATCGGGGGGCTGACCCAGCTCTGCTCCAGGAGATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 2  
US-09-030-607-173  
Sequence 173, Application US/09030607  
Patent No. 6262245  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,607  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121,427C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 173:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-030-607-173

Alignment Scores:  
Pred. No.: 4,3e-79 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0

US-10-726-093-10 (1-146) x US-09-030-607-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAGAAAGCAATGTTCTGCTGGGCGTCTGTCATCCGACGTGGTCTCTCAGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40  
DB 100 GCACACTGTTTCCAGAACTCTACACATCCGGGCTGGCTGCAGACACTTTCAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGlnAlaSerLeuSerValArgHisProGlnTrpValAsn 60  
DB 160 CAAGAGCCAGGAGCGAGATGTGTGAGGCGAGCTCTCCGTACGGACCCAGAGTACAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnSer 80  
DB 220 AGACCTTCTGCTGCTAACGACCTCATGCTCATCAAGTGTGAGACGATCCGTCTCCAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlnAsnSerCysLeu 100  
DB 280 GACACCATCCGAGCATGACATGCTTCGCAAGTCCCTACCGGGGAACTTTCCTCCTC 339  
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGlnLeuThrGlyValLysLeuProSerSer 120  
DB 340 GTTTCGTGGCTGGGCTGCTGCGGAACTGAGCTACGAGTGTGTCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlnCys 140  
DB 400 AGAAGGTCTCTGCTGACGATCGGGGGGCTGACCCAGACTCTGCTCCAGGAGATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 3  
US-09-439-313-173  
Sequence 173, Application US/09439313  
Patent No. 6329505  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reiter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42709
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1265)
; OTHER INFORMATION: n = A,T,C or G
; US-09-439-313-173

Alignment Scores:
Pred. No.: 4.3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-439-313-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAGCAATGTTGCTCGGCGCTCTGTCATCCGACAGTGGTGTGAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGCTGGGCTGCACACTCTTGAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyra 60
DB 160 CAAGAGCCAGGAGCCAGATGTGAGAGCCAGCCTCCGTACGGCACCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGTCTCTTAACGACCTCATGCTCATCAAGTTGACGAATCCGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGACATCAGCATTTCTCCAGTGCCTTACCGGGGAACCTTTCCTC 339
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTCGGCTGGGGTGTGCTGGGAAAGTGAGCTCAGGAGTGTGTCTGCCCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTTCCCGCAGTCCGGGGGCTGACCCAGAGCTGTGCTCCAGGAGAAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAGTGCG 477

RESULT 4
US-09-352-616A-173
; Sequence 173, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
```

```

; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.42709
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1265)
; OTHER INFORMATION: n = A,T,C or G
; US-09-352-616A-173

Alignment Scores:
Pred. No.: 4.3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-352-616A-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAAGCAATGTTGCTCGGCGCTCTGTCATCCGACAGTGGTGTGAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGCTGGGCTGCACACTCTTGAGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyra 60
DB 160 CAAGAGCCAGGAGCCAGATGTGAGAGCCAGCCTCCGTACGGCACCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AACCTTGTCTCTTAACGACCTCATGCTCATCAAGTTGACGAATCCGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGACATCAGCATTTCTCCAGTGCCTTACCGGGGAACCTTTCCTC 339
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTTCGGCTGGGGTGTGCTGGGAAAGTGAGCTCAGGAGTGTGTCTGCCCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTTCCCGCAGTCCGGGGGCTGACCCAGAGCTGTGCTCCAGGAGAAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAGTGCG 477

RESULT 5
US-09-232-149A-173
; Sequence 173, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
```

```
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232.149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-173
```

## Alignment Scores:

Pred. No.:	4.3e-79	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-726-093-10 (1-146) x US-09-232-149A-173 (1-1265)

```
QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGAAACGAAATGTTCTGCTCGGGCGTCTGTGCATCCGACAGGGGTCTGTCAAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCAATCGGGCTGGGCTTCAAGTCTTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyTrAsn 60
DB 160 CAAAGCCAGGAGACCAAGATGTGTGAGAGCCAGCTCTCCGTACGGACCCAGAGTACAAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTGCTTACGACCTCATGCTCAAGTTGAGCAATCCGTGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGATCGACATGCTTGCAGATGCCCTTACCGGGGAACTTTGCTCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGTGGGTCTGCTGCGAAGCGGTGAGCTCACGGGTGTGTGTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgIleGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCGCAGTCGCGGGGCTGACCCAGAGCTTGTGCTCCAGGACAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAATGCG 477
```

## RESULT 6

```
US-09-159-812-173
Sequence 173, Application US/09159812A
Patent No. 6613872
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
FILE REFERENCE: 210121.428C5
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
```

```
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-159-812-173
```

## Alignment Scores:

Pred. No.:	4.3e-79	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-726-093-10 (1-146) x US-09-159-812-173 (1-1265)

```
QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGAAACGAAATGTTCTGCTCGGGCGTCTGTGCATCCGACAGGGGTCTGTCAAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACCAATCGGGCTGGGCTTCAAGTCTTGAGGCCGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyTrAsn 60
DB 160 CAAAGCCAGGAGACCAAGATGTGTGAGAGCCAGCTCTCCGTACGGACCCAGAGTACAAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTGCTTACGACCTCATGCTCAAGTTGAGCAATCCGTGTCCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGATCGACATGCTTGCAGATGCCCTTACCGGGGAACTTTGCTCTC 339
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGGGTGGGTCTGCTGCGAAGCGGTGAGCTCACGGGTGTGTGTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgIleGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCGCAGTCGCGGGGCTGACCCAGAGCTTGTGCTCCAGGACAGATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAATGCG 477
```

## RESULT 7

```
US-09-636-215-173
Sequence 173, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```



TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.42717C17  
 CURRENT APPLICATION NUMBER: US/09/636,215  
 CURRENT FILING DATE: 2000-08-10  
 NUMBER OF SEQ ID NOS: 852  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO 173  
 LENGTH: 1265  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)...(1265)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-636-215-173

Alignment Scores:  
 Pred. No.: 4,3e-79 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 Gaps: 0

US-10-726-093-10 (1-146) x US-09-636-215-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAAAAGAAATGTTCTGCTCGGCGCTCTGTCATCCGACAGGGGTGTCAGAGC 99  
 QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40  
 DB 100 GCACACTGTTCCAGAACTCTACACCATCGGGCTGGCTGACAGTCTTGAAGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
 DB 160 CAAGAGCCAGAGGAGCCAGATGTGAGAGCCAGCTCTCGTACGAGCACCAGATACAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGCTGCTTACACCTCACTGCTCATCAATTGGACGAATCCGCTCCAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCATCGGAGCATGACATTGCTCGACAGTCCCTACCCGGGGAATCTTCCCTC 339  
 QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTCTGGCTGGGGTCTGCTGGGGAACGGTGAGCTCAAGGAGTGTGTGCTCCCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGGAGGTCTCTGCTCCAGTCCGAGGAGGCTGACCCAGAGCTCTGCTCCAGGAGATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTCTGCAGTGGC 477

RESULT 8  
 US-09-685-166A-173  
 Sequence 173, Application US/09685166A  
 Patent No. 6630305  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Jjiang, Yugu  
 APPLICANT: Henderson, Robert A.  
 APPLICANT: Kalos, Michael D.  
 APPLICANT: Fanger, Gary R.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.  
 APPLICANT: Vedvick, Thomas S.  
 APPLICANT: Carter, Darrick  
 APPLICANT: Li, Samuel  
 APPLICANT: Wang, Aijun  
 APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Hepler, William  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.427C21  
 CURRENT APPLICATION NUMBER: US/09/685,166A  
 CURRENT FILING DATE: 2000-10-10  
 NUMBER OF SEQ ID NOS: 898  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO 173  
 LENGTH: 1265  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)...(1265)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-685-166A-173

Alignment Scores:  
 Pred. No.: 4,3e-79 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 Gaps: 0

US-10-726-093-10 (1-146) x US-09-685-166A-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAAAAGAAATGTTCTGCTCGGCGCTCTGTCATCCGACAGGGGTGTCAGAGC 99  
 QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40  
 DB 100 GCACACTGTTCCAGAACTCTACACCATCGGGCTGGCTGACAGTCTTGAAGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
 DB 160 CAAGAGCCAGAGGAGCCAGATGTGAGAGCCAGCTCTCGTACGAGCACCAGATACAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGCTGCTTACACCTCACTGCTCATCAATTGGACGAATCCGCTCCAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCATCGGAGCATGACATTGCTCGACAGTCCCTACCCGGGGAATCTTCCCTC 339  
 QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTCTGGCTGGGGTCTGCTGGGGAACGGTGAGCTCAAGGAGTGTGTGCTCCCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGGAGGTCTCTGCTCCAGTCCGAGGAGGCTGACCCAGAGCTCTGCTCCAGGAGATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTCTGCAGTGGC 477

RESULT 9  
 US-09-115-453-173  
 Sequence 173, Application US/09115453B  
 Patent No. 6657056  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.

```

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1265)
; OTHER INFORMATION: n = A,T,C or G
US-09-115-453-173

Alignment Scores:
Pred. No.: 4,3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-115-453-173 (1-1265)

Qy 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db 40 ATGGAAAACGAATTTCTGCTCGGCGCTGCTGTCATCCGACATGGGTGTCGTCACCC 99
Qy 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCCCTGCACAGTCTGAGGCCAC 159
Qy 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
Db 160 CAAAGGCCAAGGAGCCAGATGTGTGAGGCCACCTCTCCGTAAGCCAGACCAAGTACAC 219
Qy 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleTyrLeuAspGluSerValSerGluSer 80
Db 220 AGACCTTGTCTGCTTACGACCTTCACTGCTCATGTAAGATCCGTGTCGACGTCCT 279
Qy 81 AspThrIleArgSerIleSerIleAsnSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db 280 GACACCATCCGAGCATGAGCATGCTTCCGACGTCCTTACCGCGGGAACCTTGCCTC 339
Qy 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120
Db 340 GTTTCGTGGGTGGGTCTGCTGCGAAGCGGTGAGCTCAGGGTGTGTCTGCCCTCTTCA 399
Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 400 AGGAGTCTCTGCGCCAGTCGCGGGGCTGACCCAGAGCTGCTCCAGGACGAATGC 459
Qy 141 LeuProCysCysSerAla 146
Db 460 CTACCGTGTGCAAGTGC 477

RESULT 10
US-09-688-489-173
; Sequence 173, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1265)
; OTHER INFORMATION: n = A,T,C or G
US-09-688-489-173

Alignment Scores:
Pred. No.: 4,3e-79 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-688-489-173 (1-1265)

Qy 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db 40 ATGGAAAACGAATTTCTGCTCGGCGCTGCTGTCATCCGACATGGGTGTCGTCACCC 99
Qy 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCCCTGCACAGTCTGAGGCCAC 159
Qy 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
Db 160 CAAAGGCCAAGGAGCCAGATGTGTGAGGCCACCTCTCCGTAAGCCAGACCAAGTACAC 219
Qy 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleTyrLeuAspGluSerValSerGluSer 80
Db 220 AGACCTTGTCTGCTTACGACCTTCACTGCTCATGTAAGTGAAGATCGTTCGAGTCT 279
Qy 81 AspThrIleArgSerIleSerIleAsnSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db 280 GACACCATCCGAGCATGAGCATGCTTCCGACGTCCTTACCGCGGGAACCTTGCCTC 339
Qy 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120
Db 340 GTTTCGTGGGTGGGTCTGCTGCGAAGCGGTGAGCTCAGGGTGTGTCTGCCCTCTTCA 399
Qy 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
Db 400 AGGAGTCTCTGCGCCAGTCGCGGGGCTGACCCAGAGCTTGTGCTCCAGGACGAATGC 459
Qy 141 LeuProCysCysSerAla 146
Db 460 CTACCGTGTGCAAGTGC 477

RESULT 11
US-09-679-426-173
; Sequence 173, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
```

APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Hepler, William  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.427C20  
 CURRENT APPLICATION NUMBER: US/09/679,426  
 CURRENT FILING DATE: 2000-10-02  
 NUMBER OF SEQ ID NOS: 895  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 173  
 LENGTH: 1265  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(1265)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-679-426-173

Alignment Scores:  
 Pred. No.: 4.3e-79 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 Gaps: 0  
 DB: 3

US-10-726-093-10 (1-146) x US-09-679-426-173 (1-1265)

QY 1 MetGluAnGluLeuPheCySerGlyValLeuValHisProGIntPValLeuSerAla 20  
 DB 40 ATGAAACGAATGTTCTGCTCGGCGCTCTGTCGTCATCCGACATGGGTCTGTACACC 99  
 QY 21 AlaHisCySPheGlnAAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
 DB 100 GCACACTGTTTCCAAACTCTTACACCATCGGCTGGGCTGTCACAGCTTGAGGCCAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGIntPVal 60  
 DB 160 CAAGAGCCAGGAGCAGATGTTGAGGCGACCTCTCGTACGCGACCCAGATACAAAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGTCTGCTACAGCACTCTCATGCTCATCAAGTTGAGCAATCGTGTCCAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAAsnSerCysLeu 100  
 DB 280 GACACCATCCGAGATCAGCATGCTTGCAGTGCCCTTACCGCGGGAACCTTGCTTC 339  
 QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTTCGTGGCTGGGCTGTGTCGGAACGCTGACGGGTGTGTCTGCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGAGGTCTCTGCGCAGTCGGGGGCTGACCCAGACGCTTGTGCTCCAGAGAGATGC 459  
 QY 141 LeuProCyCySerSerAla 146  
 DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 12  
 US-09-759-143-173  
 Sequence 173, Application US/09759143

Patent No. 6800746  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Devin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Jiang, Yugu  
 APPLICANT: Henderson, Robert A.  
 APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Stolk, John A.  
 APPLICANT: Day, Craig H.  
 APPLICANT: Vedvick, Thomas S.  
 APPLICANT: Carter, Darrick  
 APPLICANT: Li, Samuel  
 APPLICANT: Wang, Aijun  
 APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Hepler, William  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.427C23  
 CURRENT APPLICATION NUMBER: US/09/759,143  
 CURRENT FILING DATE: 2001-01-12  
 NUMBER OF SEQ ID NOS: 934  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 173  
 LENGTH: 1265  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(1265)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-759-143-173

Alignment Scores:  
 Pred. No.: 4.3e-79 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 Gaps: 0  
 DB: 3

US-10-726-093-10 (1-146) x US-09-759-143-173 (1-1265)

QY 1 MetGluAnGluLeuPheCySerGlyValLeuValHisProGIntPValLeuSerAla 20  
 DB 40 ATGAAACGAATGTTCTGCTCGGCGCTCTGTCGTCATCCGACATGGGTCTGTACACC 99  
 QY 21 AlaHisCySPheGlnAAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
 DB 100 GCACACTGTTTCCAAACTCTTACACCATCGGCTGGGCTGTCACAGCTTGAGGCCAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGIntPVal 60  
 DB 160 CAAGAGCCAGGAGCAGATGTTGAGGCGACCTCTCGTACGCGACCCAGATACAAAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGTCTGCTACAGCACTCTCATGCTCATCAAGTTGAGCAATCGTGTCCAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAAsnSerCysLeu 100  
 DB 280 GACACCATCCGAGATCAGCATGCTTGCAGTGCCCTTACCGCGGGAACCTTGCTTC 339  
 QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTTCGTGGCTGGGCTGTGTCGGAACGCTGACGGGTGTGTCTGCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGAGGTCTCTGCGCAGTCGGGGGCTGACCCAGACGCTTGTGCTCCAGAGAGATGC 459  
 QY 141 LeuProCyCySerSerAla 146  
 DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 13  
 US-09-651-236-173  
 Sequence 173, Application US/09651236  
 Patent No. 6818751

GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.42718C18  
CURRENT APPLICATION NUMBER: US/09/651.236  
CURRENT FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 865  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 173  
LENGTH: 1265  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1265)  
OTHER INFORMATION: n = A,T,C or G  
US-09-651-236-173

Alignment Scores:  
Pred. No.: 4.3e-79 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-651-236-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAGAAAGCAATTGTTCTGCTGGGCGTCTGTCATCCGACGTGGTCTGTACGCC 99

QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACGTTTCCAGAACTCCTACACCATCGGGCTGGCGACAGTCTTGAGGCCGAC 159

QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaGhisProGlnTyrAsn 60  
DB 160 CAAGAGCCAGAGGAGCCAGATGGTGAGCGACGCTCTCCCTACGCGACCCAGAGTACAC 219

QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGCTGCTGTAACGACCTATGCTCATCAAGTTGACGAATCCGTGTCGAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCCATCCGAGACATCACATGCTTCCAGAGGCTTCCGCGGAGAACTTGCTCTC 339

QY 101 ValSerGlyTyrProGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTTCGTGGGTGGGTCTGCTGGCCAGCGTAGCTCAAGGGTGTCTGCTCTTCA 359

QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGAGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459

QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCGAGTGGC 477

RESULT 14  
US-09-030-606-173  
Sequence 173, Application US/09030606  
Patent No. 6887660  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,606  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Waki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.428C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 173:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-030-606-173

Alignment Scores:  
Pred. No.: 4.3e-79 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-030-606-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAGAAAGCAATTGTTCTGCTGGGCGTCTGTCATCCGACGTGGTCTGTACGCC 99

QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACGTTTCCAGAACTCCTACACCATCGGGCTGGCGACAGTCTTGAGGCCGAC 159

QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaGhisProGlnTyrAsn 60  
DB 160 CAAGAGCCAGAGGAGCCAGATGGTGAGCGACGCTCTCCCTACGCGACCCAGAGTACAC 219

QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGCTGCTGTAACGACCTATGCTCATCAAGTTGACGAATCCGTGTCGAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
|||  
DB 280 GACACCATCCGGAGCATCAGCATGCTTCCAGAGCCCTACCGGGGGAATCTTGCTC 339  
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGlnLeuThrGlyValCysLeuProSerSer 120  
|||  
DB 340 GTTCTGTGGCTGGGGTCTGCTGGCGAACGGTGAAGCTACGGGTGTGTCTGCTTCA 399  
QY 121 ArgArgSerSerIleArgIleSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140  
|||  
DB 400 AGAGGTCCTCTGCTCCAGCTCCGGGGGCTGACCAAGCTCTGCTCCAGGCAAGATGC 459  
QY 141 LeuProCysCysSerAla 146  
|||  
DB 460 CTACCGTCTGCAGTGGC 477  
RESULT 15.  
US-09-657-279-173  
; Sequence 173, Application US/09657279  
; Patent No. 6894146  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kaios, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stoik, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Derrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C19  
; CURRENT FILING DATE: 2000-09-06  
; NUMBER OF SEQ ID NOS: 877  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 173  
; LENGTH: 1265  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1265)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-657-279-173  
Alignment Scores:  
Pred. No.: 4,3e-79 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0  
US-10-726-093-10 (1-146) x US-09-657-279-173 (1-1265)  
QY 1 MetGluAsnGlnLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
|||  
DB 40 ATGGAAGAAAGAAATGTTCTGCTGGCGGCTCTGGTGCAATCCGAGTGGGTGCTGAGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40  
|||  
DB 100 GCAGACTGTTCCAGAACTCTACACCATGGGCTGGGCTGCAAGCTCTTGAAGCGAGC 159

QY 41 GlnGluProGlySerGlnMetValGlnAlaSerLeuSerValArgHisProGlnTrpAsn 60  
|||  
DB 160 CAGAGCCAGGAGCCAGATGTGGAGGCCAGGCTCTCCGTAGGCAACCCAGATCAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGlnSerValSerGlnSer 80  
|||  
DB 220 AGACCTTGCTCGCTAAGCACTCATGCTCATCAAGTTGAGCAAAATCCGTTCCAGACT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
|||  
DB 280 GACACCATCCGGAGCATCAGCATGCTTCCAGTGCCTTACCGCGGGAATCTTGCTC 339  
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGlnLeuThrGlyValCysLeuProSerSer 120  
|||  
DB 340 GTTCTGTGGCTGGGGTCTGCTGGGAACGGTGAAGCTACGGGTGTGTCTGCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140  
|||  
DB 400 AGAGGTCCTCTGCTCCAGTGCAGGGGGCTGACCAAGCTCTGCTCCAGGCAAGATGC 459  
QY 141 LeuProCysCysSerAla 146  
|||  
DB 460 CTACCGTCTGCAGTGGC 477

Search completed: August 28, 2006, 18:28:06  
Job time : 152 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 28, 2006, 18:26:14 ; Search time 1073 Seconds  
(without alignments)  
2507.914 Million cell updates/sec

Title: US-10-726-093-10

Perfect score: 758  
Sequence: 1 MENELFCGSLVHPQWLSA.....SRGLTSSASQAELPCCSA 146

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-DB=abs/ABSSWB.spool/US10726093.rnphm 28082006 121147 25953/app.query.fasta\_1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TPANS=human40.csl -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abs808  
-USER=US10726093 @CN 1 1 1675 @runat 28082006 121147 25953 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WAPRO TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	758	100.0	702	10	US-10-726-093-3

Result No.	Score	Query Match	Length DB	ID	Description
1	758	100.0	702	10	US-10-726-093-3
2	758	100.0	702	10	US-10-726-093-3
3	758	100.0	702	10	US-10-726-093-3
4	758	100.0	702	10	US-10-726-093-3
5	758	100.0	702	10	US-10-726-093-3
6	758	100.0	702	10	US-10-726-093-3
7	758	100.0	702	10	US-10-726-093-3
8	758	100.0	702	10	US-10-726-093-3
9	758	100.0	702	10	US-10-726-093-3
10	758	100.0	702	10	US-10-726-093-3
11	758	100.0	702	10	US-10-726-093-3
12	758	100.0	702	10	US-10-726-093-3
13	758	100.0	702	10	US-10-726-093-3
14	758	100.0	702	10	US-10-726-093-3
15	758	100.0	702	10	US-10-726-093-3
16	758	100.0	702	10	US-10-726-093-3
17	758	100.0	702	10	US-10-726-093-3
18	758	100.0	702	10	US-10-726-093-3
19	758	100.0	702	10	US-10-726-093-3
20	758	100.0	702	10	US-10-726-093-3
21	758	100.0	702	10	US-10-726-093-3
22	758	100.0	702	10	US-10-726-093-3
23	758	100.0	702	10	US-10-726-093-3
24	758	100.0	702	10	US-10-726-093-3
25	758	100.0	702	10	US-10-726-093-3
26	758	100.0	702	10	US-10-726-093-3
27	758	100.0	702	10	US-10-726-093-3
28	758	100.0	702	10	US-10-726-093-3
29	758	100.0	702	10	US-10-726-093-3
30	758	100.0	702	10	US-10-726-093-3
31	758	100.0	702	10	US-10-726-093-3
32	758	100.0	702	10	US-10-726-093-3
33	758	100.0	702	10	US-10-726-093-3
34	758	100.0	702	10	US-10-726-093-3
35	758	100.0	702	10	US-10-726-093-3
36	758	100.0	702	10	US-10-726-093-3
37	758	100.0	702	10	US-10-726-093-3
38	758	100.0	702	10	US-10-726-093-3
39	758	100.0	702	10	US-10-726-093-3
40	758	100.0	702	10	US-10-726-093-3
41	758	100.0	702	10	US-10-726-093-3
42	758	100.0	702	10	US-10-726-093-3
43	758	100.0	702	10	US-10-726-093-3
44	758	100.0	702	10	US-10-726-093-3
45	758	100.0	702	10	US-10-726-093-3

#### ALIGNMENTS

RESULT 1  
US-10-726-093-3  
Publication 3, Application US/10726093  
Publication No. US20050106643A1  
GENERAL INFORMATION:  
APPLICANT: Satcloglu, Fahri  
TITLE OF INVENTION: Differentially Expressed Genes in  
Prostate Cancer  
FILE REFERENCE: 50218/002003  
CURRENT APPLICATION NUMBER: US/10/726, 093  
CURRENT FILING DATE: 2003-12-01  
PRIOR APPLICATION NUMBER: US/09/743, 682  
PRIOR FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: PCT/IB00/00673  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: US 60/135, 325  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 60/135, 333  
PRIOR FILING DATE: 1999-05-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.10  
SEQ ID NO 3  
LENGTH: 702  
TYPE: DNA  
ORGANISM: Homo sapiens

US-10-726-093-3

Alignment Scores:  
Pred. No.: 1,35e-87 Length: 702  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 10 Gaps: 0

US-10-726-093-10 (1-146) x US-10-726-093-3 (1-702)

```
OY 1 MetGluasnGluLeuPheCysSerGlyValLeuValHisProGlnITrpValLeuSerAla 20
DB 1 ATGGAAGAAAGAAATGTTCTGCTCGGGCGTCTGTCATCCGACAGTGGTCTGTCCAGCC 60
OY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 61 GCACACTGTTCCAGAACTCTTACACCATCGGGCTGGCCCTCACAGTCTTGAGGCCGAC 120
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnITyrAsn 60
DB 121 CAAGAGCCAGGAGCCAGATGTGGAGGCCAGCTCTCCGTACGGCACCAGATGACAC 180
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 181 AGACCTTGCTCGCTTACGACCTCATCTCAAGTTGACGAAATCCGTGCCAGTCT 240
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 241 GACACCATCCGAGAGCATGACATTCCTTCGACGTGCCCTTACCGGGGAACTTTGGCCCTC 300
OY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 301 GTTTCGGCTGGGGTCTGCTGGGAAACGCTGACCTACCGGTGTGTCTGCCCTTTCA 360
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 361 AGGAGTCTCTCTGCCAGTCCGGGGGCTGACCCAGAGCTCTGCCGCCAGGAGAAATGC 420
OY 141 LeuProCysCysSerAla 146
DB 421 CTACCGTCTGCGACGTGCG 438
```

RESULT 2

US-10-473-485-1  
Sequence 1, Application US/10473485  
Publication No. US20040137455A1  
GENERAL INFORMATION:  
APPLICANT: Clements, Judith A  
APPLICANT: Dong, Ying  
TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign  
FILE REFERENCE: DAV1172.00/4APC  
CURRENT FILING DATE: 2003-09-29  
PRIOR APPLICATION NUMBER: US/10/473,485  
PRIOR FILING DATE: 2001-03-27  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 848  
TYPE: DNA  
ORGANISM: human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(585)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: (586)..(847)  
OTHER INFORMATION:  
US-10-473-485-1

Alignment Scores:

Pred. No.: 1,75e-87 Length: 848  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0

US-10-726-093-10 (1-146) x US-10-473-485-1 (1-848)

```
OY 1 MetGluasnGluLeuPheCysSerGlyValLeuValHisProGlnITrpValLeuSerAla 20
DB 148 ATGGAAGAAAGAAATGTTCTGCTCGGGCGTCTGTCATCCGACAGTGGTCTGTCCAGCC 207
OY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 208 GCACACTGTTCCAGAACTCTTACACCATCGGGCTGGCCCTCACAGTCTTGAGGCCGAC 267
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnITyrAsn 60
DB 268 CAAGAGCCAGGAGCCAGATGTGGAGGCCAGCTCTCCGTACGGCACCAGATGACAC 327
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 328 AGACCTTGCTCGCTTACGACCTCATCTCAAGTTGACGAAATCCGTGCCAGTCT 387
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 388 GACACCATCCGAGAGCATGACATTCCTTCGACGTGCCCTTACCGGGGAACTTTGGCCCTC 447
OY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 448 GTTTCGGCTGGGGTCTGCTGGGAAACGCTGACCTACCGGTGTGTCTGCCCTTTCA 507
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 508 AGGAGTCTCTCTGCCAGTCCGGGGGCTGACCCAGAGCTCTGCCGCCAGGAGAAATGC 567
OY 141 LeuProCysCysSerAla 146
DB 568 CTACCGTCTGCGACGTGCG 585
```

RESULT 3

US-09-759-143-173  
Sequence 173, Application US/09759143  
Patent No. US2002022248A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yaser A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C23  
CURRENT APPLICATION NUMBER: US/09/759,143  
CURRENT FILING DATE: 2001-01-12  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 173  
LENGTH: 1265



TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1265)  
OTHER INFORMATION: n = A,T,C or G  
US-09-759-143-173

Alignment Scores:  
Pred. No.: 3,05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-759-143-173 (1-1265)

QY 1 MetGluASrGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAAGCAATTTCTTCTGCTGGGCGTCTGTCATCCGACGGGTGCTGACGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTTCAGAACTCTACACCACTCGGCTGGCTGCACTCTTGAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpValLeuSerAla 60  
DB 160 CAAGAGCCAGGAGCCAGATGTTGAGAGCCAGCTCTCCGTACGGCAGCCAGATCAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTCTGCTCTAAGCACTCATGCTCATCAAGTTGACCAATCCGTCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGAGCATGCTGCTGCGAGTCCCTACCGGGGAACTTTGCTC 339  
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTCTGCTGGGGTCTGCTGCGGAAACGTGAGCTCAAGGTTGTCTGCTGCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGGAGGTCTCTCTCCCACTGCGGGGCTGACCCAGAGCTCTGCTCCAGGAGATGC 459  
QY 141 LeuProCysSerSerAla 146  
DB 460 CTACCGTCTGCACTGCG 477

# RESULT 4

US-09-780-669-173

Sequence 173, Application US/09780669

Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jianshun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Scolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedavick, Thomas S.

APPLICANT: Carter, Darick

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

APPLICANT: Hural, John

APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C24  
CURRENT APPLICATION NUMBER: US/09/780.669  
CURRENT FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 943  
SOFTWARE: PasteSeq for Windows Version 3.0  
SEQ ID NO: 173  
LENGTH: 1265  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1265)  
OTHER INFORMATION: n = A,T,C or G  
US-09-780-669-173

Alignment Scores:  
Pred. No.: 3,05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-10-726-093-10 (1-146) x US-09-780-669-173 (1-1265)

QY 1 MetGluASrGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAAGCAATTTCTTCTGCTGGGCGTCTGTCATCCGACGGGTGCTGACGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTTCAGAACTCTACACCACTCGGCTGGCTGCACTCTTGAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpValLeuSerAla 60  
DB 160 CAAGAGCCAGGAGCCAGATGTTGAGAGCCAGCTCTCCGTACGGCAGCCAGATCAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTCTGCTCTAAGCACTCATGCTCATCAAGTTGACCAATCCGTCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGAGCATGCTGCTGCGAGTCCCTACCGGGGAACTTTGCTC 339  
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTCTGCTGGGGTCTGCTGCGGAAACGTGAGCTCAAGGTTGTCTGCTGCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGGAGGTCTCTCTCCCACTGCGGGGCTGACCCAGAGCTCTGCTCCAGGAGATGC 459  
QY 141 LeuProCysSerSerAla 146  
DB 460 CTACCGTCTGCACTGCG 477

# RESULT 5

US-09-030-606-173

Sequence 173, Application US/09030606

Patent No. US20020081580A1

GENERAL INFORMATION:

APPLICANT: Xu, Jianshun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS

NUMBER OF SEQUENCES: 224

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,606  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.428C3  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 173:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-030-606-173

Alignment Scores:  
Pred. No.: 3,05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
US-10-726-093-10 (1-146) x US-09-030-606-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValIleuValHisProGlnTrpValIleuSerAla 20  
DB 40 ATGGAAACGAATGTTCTGCTCGGCGCTCGGTGCATCCCGAGGGGTGCTGTCAGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTACACCATCGGCTGGGCTGACAGTCTTGAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 160 CAAGAGCCAGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGCGACCCAGAGTACAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGlnSerValSerGluSer 80  
DB 220 AACACCTTCTCGCTAACACCTCATCATCAAGTTGAGCAATCCGTTGTCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlnAsnSerCysLeu 100  
DB 280 GACACCATCCGAGACATCAGCATTCCTTCGCACTGCCCTACCCGGGGAACCTTCCCTC 339  
QY 101 ValSerGlyTyrPglYleuLeuAlaAsnGlyGluLeuThrGlyValAlaCysLeuProSerSer 120  
DB 340 GTTTCGGCTGGGCTGCTGCTGGGGAACGGTGAAGCTCAGCGGTGTGTGCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGAGAGTCTCTGCTCCAGTGGCGGGGCTGACCCAGAGCTCTGCGTCCAGGAGAAATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCAAGTGGC 477

RESULT 6  
US-09-822-827-173  
; Sequence 173, Application US/09822827  
; Patent No. US20020081680A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.534C1  
; CURRENT APPLICATION NUMBER: US/09/822,827  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 173  
; LENGTH: 1265  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1265)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-822-827-173

Alignment Scores:  
Pred. No.: 3,05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
US-10-726-093-10 (1-146) x US-09-822-827-173 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValIleuValHisProGlnTrpValIleuSerAla 20  
DB 40 ATGGAAACGAATGTTCTGCTCGGCGCTCGGTGCATCCCGAGGGGTGCTGTCAGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTACACCATCGGCTGGGCTGACAGTCTTGAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 160 CAAGAGCCAGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGCGACCCAGAGTACAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGlnSerValSerGluSer 80  
DB 220 AACACCTTCTCGCTAACACCTCATCATCAAGTTGAGCAATCCGTTGTCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlnAsnSerCysLeu 100  
DB 280 GACACCATCCGAGACATCAGCATTCCTTCGCACTGCCCTACCCGGGGAACCTTCCCTC 339  
QY 101 ValSerGlyTyrPglYleuLeuAlaAsnGlyGluLeuThrGlyValAlaCysLeuProSerSer 120  
DB 340 GTTTCGGCTGGGCTGCTGCTGGGGAACGGTGAAGCTCAGCGGTGTGTGCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGAGAGTCTCTGCTCCAGTGGCGGGGCTGACCCAGAGCTCTGCGTCCAGGAGAAATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCAAGTGGC 477  
RESULT 7  
US-09-115-453-173  
; Sequence 173, Application US/09115453B  
; Patent No. US20020090372A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

;; TITLE OF INVENTION: METHODS FOR THEIR USE  
;; FILE REFERENCE: 210121.427C4  
;; CURRENT APPLICATION NUMBER: US/09/115.453B  
;; CURRENT FILING DATE: 1998-07-14  
;; NUMBER OF SEQ ID NOS: 228  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 173  
;; LENGTH: 1265  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(1265)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-115-453-173

Alignment Scores:  
Pred. No.: 3,05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0

US-10-726-093-10 (1-146) x US-09-115-453-173 (1-1265)

QY 1 MetGluAenGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAACGAATTGTTCTGCTCGGAGCTCTGCTGTCATCCGACAGGCTGCTGACGC 99  
QY 21 AlaHisCySPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTTACACCATCGGCTGCGCTGACAGTCTTGAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60  
DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCGAGCTCTCGTACGACCCAGATACAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
DB 220 AACCCCTTCTGCTTACGACCTCATGCTCATTAATTGGACGAATCCGTCGACGCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySeProThrAlaGlyAsnSerCySLeu 100  
DB 280 GACACCATCCGAGATCAGCATTCCTTGCAGTCCCTACCCGCGGGAATCTTCCCTC 339  
QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCySLeuProSerSer 120  
DB 340 GTTCTGCGTGGGCTGCTGCTGCGGAACGCTGAGCTCACGGGTGTGTCTGCCCCCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCyS 140  
DB 400 AGGAGGTCTCTCTCCCACTGCGGGGGCTGACCCAGAGCTCTGCTCCGACGAGATGC 459  
QY 141 LeuProCySeSerAla 146  
DB 460 CTACCGTCTGCAAGTCCG 477

RESULT 8  
US-09-232-880-173  
; Sequence 173, Application US/09232880  
; Publication No. US20020182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
; FILE REFERENCE: 210121.428C6  
; CURRENT APPLICATION NUMBER: US/09/232.880  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 173  
;; LENGTH: 1265  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(1265)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-232-880-173

Alignment Scores:  
Pred. No.: 3,05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0

US-10-726-093-10 (1-146) x US-09-232-880-173 (1-1265)

QY 1 MetGluAenGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAACGAATTGTTCTGCTCGGAGCTCTGCTGTCATCCGACAGGCTGCTGACGC 99  
QY 21 AlaHisCySPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTTACACCATCGGCTGCGCTGACAGTCTTGAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60  
DB 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCGAGCTCTCGTACGACCCAGATACAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
DB 220 AACCCCTTCTGCTTACGACCTCATGCTCATTAATTGGACGAATCCGTCGACGCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySeProThrAlaGlyAsnSerCySLeu 100  
DB 280 GACACCATCCGAGATCAGCATTCCTTGCAGTCCCTACCCGCGGGAATCTTCCCTC 339  
QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCySLeuProSerSer 120  
DB 340 GTTCTGCGTGGGCTGCTGCTGCGGAACGCTGAGCTCACGGGTGTGTCTGCCCCCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCyS 140  
DB 400 AGGAGGTCTCTCTCCCACTGCGGGGGCTGACCCAGAGCTCTGCTCCGACGAGATGC 459  
QY 141 LeuProCySeSerAla 146  
DB 460 CTACCGTCTGCAAGTCCG 477

RESULT 9  
US-09-895-793-173  
; Sequence 173, Application US/09895793  
; Publication No. US20020192763A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.

```

APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-895-793-173

Alignment Scores:
Pred. No.: 3.05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-726-093-10 (1-146) x US-09-895-793-173 (1-1265)
QY 1 MetGluAnGluLeuPheCySeRGlyValLeuValHisProGIntRpValLeuSerAla 20
DB 40 ATGAAACCAATTTGTTCTGCTCGGGGCTCTGTGTCATCCGAGTGGTGCTGTCAACC 99
QY 21 AlaHisCySPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGGCGACACAGCTTGAGGCGGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB 160 CAAAGCCAGGAGCCAGATGATGAGGCGACGCTCTCCGACCGGACCCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTGCTAACGACTCATGCTCATCAAGTTGGACGAATCCGTCTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGATCAGCATTCCTCGCAGTGCCTTACCGGGGAACTTTGCTTC 339
QY 101 ValSerGlyTyrPglYLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGCTGGGCTGCTGCTGCGAACGCTGACGAGTGTGTCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCGCCACTCCGGGGGCTGACCCAGACTCTGCGTCCCAAGCAATGC 459
QY 141 LeuProCyCySerAla 146
DB 460 CTACCGTGTCTGACGTGCG 477

```

## RESULT 10

```

US-09-895-814-173
Sequence 173, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.

```

```

APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 173
LENGTH: 1265
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1265)
OTHER INFORMATION: n = A,T,C or G
US-09-895-814-173

Alignment Scores:
Pred. No.: 3.05e-87 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-726-093-10 (1-146) x US-09-895-814-173 (1-1265)
QY 1 MetGluAnGluLeuPheCySeRGlyValLeuValHisProGIntRpValLeuSerAla 20
DB 40 ATGAAACCAATTTGTTCTGCTCGGGGCTCTGTGTCATCCGAGTGGTGCTGTCAACC 99
QY 21 AlaHisCySPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGGCGACACAGTCTTGAGGCGGAC 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60
DB 160 CAAAGCCAGGAGCCAGATGATGAGGCGACGCTCTCCGACCGGACCCAGAGTACAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTGCTAACGACTCATGCTCATCAAGTTGGACGAATCCGTCTCGAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGATCAGCATTCCTCGCAGTGCCTTACCGGGGAACTTTGCTTC 339
QY 101 ValSerGlyTyrPglYLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGCTGCTGGGCTGCTGCTGCGAACGCTGACGAGTGTGTCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCGCCACTCCGGGGGCTGACCCAGACTCTGCGTCCCAAGCAATGC 459

```

OY 141 LeuProCySeSerA1a 146  
DB 460 CTACCGTGTGCGAGTGGC 477

## RESULT 11

US-10-012-896-173  
Sequence 173, Application US/10012896

Publication No. US20020183251A1  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hurai, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Foy, Teresa  
APPLICANT: Fanger, Gary R.  
APPLICANT: Mantanabe, Yoshihiro  
APPLICANT: Meagher, Madeleine Joy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C27  
CURRENT APPLICATION NUMBER: US/10/012.896  
CURRENT FILING DATE: 2001-12-10  
NUMBER OF SEQ. ID NOS: 1011  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 173  
LENGTH: 1265  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 967, 1094, 1095, 1115, 1126, 1154, 1174, 1176, 1212, 1251,  
LOCATION: 1253  
OTHER INFORMATION: n = A,T,C or G  
US-10-012-896-173

## Alignment Scores:

Pred. No.: 3.05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-10-726-093-10 (1-146) x US-10-012-896-173 (1-1265)

OY 1 MetGluAsnGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerA1a 20  
DB 40 ATGAAAACGAATTGCTGCTCGGGGCTCTGTGATCGCAGTGGGTCTGTCAAGC 99  
OY 21 AlaHisCySePheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCCAGCAAGCTTGAAGCCGAC 159  
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaGHisProGluTyrrAsn 60  
DB 160 CAAAGCCAGGAGCCAGCATGATGTGAGGCGACCTCTCCGTACGGACCCAGATACAC 219

OY 61 ArgProLeuLeuAlaAsnAspLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGCTGTGCTPACACCTCAGTCATCAAGTTGAGACGATCCGTCTCCAGTCT 279  
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySeProThrAlaGlyAsnSerCyLeu 100  
DB 280 GACACCATTCGAGACATCAGCATTTGCTTGCAGTGCCCTACCCGGGGAACCTTCCCTC 339  
OY 101 ValSerGlyTyrrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCylLeuProSerSer 120  
DB 340 GTTCTGCTGGGGGTCTGCTGGCGAAACGCTGAGCTCACCGGTGTGTCTGCTTCA 399  
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCySe 140  
DB 400 AGAGGTCTCTGCGCCAGTCCGAGGCGGAGGCTGACCCAGACGCTTCCCTCCAGCAGATGC 459  
OY 141 LeuProCySeSerA1a 146  
DB 460 CTACCGTGTGCGAGTGGC 477

## RESULT 12

US-10-010-940-173  
Sequence 173, Application US/10010940

Publication No. US2003008062A1  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang Yugu  
APPLICANT: Reed, Steven G.  
APPLICANT: Kalos, Michael  
APPLICANT: Fanger, Gary  
APPLICANT: Retter, Mark  
APPLICANT: Solk, John  
APPLICANT: Day, Craig  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427D3  
CURRENT APPLICATION NUMBER: US/10/010.940  
CURRENT FILING DATE: 2001-12-05  
NUMBER OF SEQ. ID NOS: 575  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 173  
LENGTH: 1265  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..  
LOCATION: (1)..  
OTHER INFORMATION: n = A,T,C or G  
US-10-010-940-173

## Alignment Scores:

Pred. No.: 3.05e-87 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-10-726-093-10 (1-146) x US-10-010-940-173 (1-1265)

OY 1 MetGluAsnGluLeuPheCySeSerGlyValLeuValHisProGlnTrpValLeuSerA1a 20  
DB 40 ATGAAAACGAATTGCTGCTCGGGGCTCTGTGATCGCAGTGGGTCTGTCAAGC 99  
OY 21 AlaHisCySePheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGGCTGGCCAGCAAGCTTGAAGCCGAC 159  
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaGHisProGluTyrrAsn 60

DB 160 CAGAGCCCGAGGAGCCAGATGGAGGCGACCTCTTCGTACGAGGAGCCAGACAGATCAAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleYsLeuAspGluSerValSerGluSer 80  
 DB 220 AACCCCTGCTGCTACACACTCATGCTCATCACTTGGAGAAATCCGTGCTCCAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACATCCGAGAGCATGATGCTTCCAGTGCCCTACCGGGGAACTCTTGCCCTC 339  
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTCTGGCTGGGGTCTGCTGGCGAAGCGGTGAGCTCAGGGGTGTGTCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGGAGGCTCTGCTGCGCCAGTCCGGGGGCTGACCCAGAGCTTGTGCTCCAGGCAATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTCTGCAGTGCG 477  
 RESULT 13  
 US-10-144-678A-173  
 ; Sequence 173, Application US/10144678A  
 ; Publication No. US20030157089A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqiu  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stoik, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Derrick  
 ; APPLICANT: Li, Samuel X.  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A. W.  
 ; APPLICANT: Hepier, William T.  
 ; APPLICANT: Hural, John  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Houghton, Raymond L.  
 ; APPLICANT: Vinals y de Basols, Carlota  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Deng, Ta  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.427C28  
 ; CURRENT APPLICATION NUMBER: US/10/144,678A  
 ; NUMBER OF SEQ ID NOS: 1033  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 173  
 ; LENGTH: 1265  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 967\_1094, 1095, 1115, 1126, 1154, 1174, 1176, 1212, 1251,  
 ; LOCATION: 1253  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-10-144-678A-173  
 Alignment Scores:  
 Pred. No.: 3,05e-87 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0%  
 Best Local Similarity: 100.0%  
 Query Match: 7 Indels: 0  
 DB: 7 Gaps: 0

Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 7 Indels: 0  
 DB: 7 Gaps: 0  
 US-10-726-093-10 (1-146) x US-10-144-678A-173 (1-1265)  
 QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGAAAACGAATGTTCTGCTCGGCGTCTGTGATCCGACATGGGTCTGTCAACC 99  
 QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
 DB 100 GCACATGTTTCCGAACCTCTACACATCGGGCTGGGCCCTGCACAGCTTGAAGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60  
 DB 160 CAGAGCCAGGAGGACAGATGATGTGAGGCCAGCTCTCCGTAACGACAGACAGATCAAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleYsLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGTCTGCTACAGACCTCATGCTCATGAATGAGACGAATCGTGTCCAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACATCCGAGAGCATGATGCTTCCAGTGCCCTACCGGGGAACTCTTGCCCTC 339  
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTCTGGCTGGGGTCTGCTGGCGAAGCGGTGAGCTCAGGGGTGTGTCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGGAGGCTCTGCTGCGCCAGTCCGGGGGCTGACCCAGAGCTTGTGCTCCAGGCAATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTCTGCAGTGCG 477  
 RESULT 14  
 US-10-294-025-173  
 ; Sequence 173, Application US/10294025  
 ; Publication No. US20030185830A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Stoik, John A.  
 ; APPLICANT: Kalos, Michael D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.427C29  
 ; CURRENT APPLICATION NUMBER: US/10/294,025  
 ; NUMBER OF SEQ ID NOS: 1038  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 173  
 ; LENGTH: 1265  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 967\_1094, 1095, 1115, 1126, 1154, 1174, 1176, 1212, 1251,  
 ; LOCATION: 1253  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-10-294-025-173  
 Alignment Scores:  
 Pred. No.: 3,05e-87 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 7 Indels: 0  
 DB: 7 Gaps: 0

US-10-726-093-10 (1-146) x US-10-294-025-173 (1-1265)

```

OY 1 MetGluAenGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAACGAATTTCTTCTCGGCGCTCTGTCGATCCGACATGGGTCTGTCAAGC 99
OY 21 AlaHisCysPheGlnAenSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACATCGGGCTGGGGCTGCACAGTCTTGAGGCCGAC 159
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGAGCCAGGAGGACAGATGTGGAGGCGACCTCTCCGTACGGACCCAGAGTACAAAC 219
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTGCTACACACTCTCATCTCAATGAGAGAAATCCGTGCGAGGTCT 279
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGCATCAGCATTCGCTTCCATCAAGTTGAGAGAACTTTGCCCTC 339
OY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGGCTGGGGTCTGCTGGGAGACGATGAGCTCAGGATGTGTCTGCTCTTCA 399
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTGCGCCAGTCCGCGGGGCTGACCCAGACTCTGCTCCAGGAGAAATGC 459
OY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAGTCCG 477

```

RESULT 15

US-10-688-838-173

; Sequence 173, Application US/10688838

; Publication No. US20040141989A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

FILE REFERENCE: 210121.427D4

CURRENT APPLICATION NUMBER: US/10/688,838

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 173

LENGTH: 1265

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: 967, 1094, 1095, 1115, 1126, 1154, 1174, 1176, 1212, 1251,

LOCATION: 1253

OTHER INFORMATION: n = A,T,C or G

US-10-688-838-173

Alignment Scores:

Pred. No.: 3,05e-87

Score: 758.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 8

Length: 1265

Matches: 146

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-726-093-10 (1-146) x US-10-688-838-173 (1-1265)

```

OY 21 AlaHisCysPheGlnAenSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
DB 100 GCACACTGTTTCCAGAACTCTTACACATCGGGCTGGGGCTGCACAGTCTTGAGGCCGAC 159
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
DB 160 CAAGAGCCAGGAGGACAGATGTGGAGGCGACCTCTCCGTACGGACCCAGAGTACAAAC 219
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTGCTACACACTCTCATCTCAATGAGAGAAATCCGTGCGAGGTCT 279
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCATCCGAGCATCAGCATTCGCTTCCATCAAGTTGAGAGAACTTTGCCCTC 339
OY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGGCTGGGGTCTGCTGGGAGACGATGAGCTCAGGATGTGTCTGCTCTTCA 399
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGAGAGTCTCTGCGCCAGTCCGCGGGGCTGACCCAGACTCTGCTCCAGGAGAAATGC 459
OY 141 LeuProCysCysSerAla 146
DB 460 CTACCGTCTGCAGTCCG 477

```

Search completed: August 28, 2006, 18:46:07  
Job time : 1075 secs

```

OY 1 MetGluAenGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
DB 40 ATGGAAACGAATTTCTTCTCGGCGCTCTGTCGATCCGACATGGGTCTGTCAAGC 99

```



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OW protein - protein search, using sw model

Run on: August 29, 2006, 03:38:09 ; Search time 196 Seconds  
(without alignments)  
340.580 Million cell updates/sec

Title: US-10-726-093-10

Perfect score: 758  
Sequence: 1 MENELFCGVLVHPQWVLSA.....SRGLTQSSASQAELPCCSA 146

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: A\_Geneseq\_8:  
2: geneseqp1980s:  
3: geneseqp1990s:  
4: geneseqp2000s:  
5: geneseqp2001s:  
6: geneseqp2002s:  
7: geneseqp2003s:  
8: geneseqp2004s:  
9: geneseqp2005s:  
10: geneseqp2006s:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	758	100.0	146	4	AAB50449 Human pro
2	758	100.0	195	6	ABP54355 Human KTK
3	594	78.4	237	3	AAB21293 Human KTK
4	577	76.1	164	2	AAAG69389 Human KTK
5	577	76.1	164	2	AAW71873 Protein e
6	577	76.1	164	3	AAAY82006 Human imm
7	577	76.1	164	3	ABG94415 Human pro
8	577	76.1	164	4	AAAG94415 Human pro
9	577	76.1	164	4	AAU69767 Human pro
10	577	76.1	164	4	AAU69767 Human pro
11	577	76.1	164	4	AAU69767 Human pro
12	577	76.1	164	4	AAU69767 Human pro
13	577	76.1	164	4	AAU69767 Human pro
14	577	76.1	164	5	ABP54355 Human pro
15	577	76.1	164	5	ABP54355 Human pro
16	577	76.1	164	6	ABP54355 Human pro
17	577	76.1	164	6	ABP54355 Human pro
18	577	76.1	164	7	ADG26044 Human pro
19	577	76.1	164	10	AEF6325 Human pro
20	577	76.1	205	4	AAAY82006 Human pro
21	577	76.1	220	3	AAAY82008 Human imm
22	577	76.1	220	4	AAU69768 Human pro
23	577	76.1	220	4	AAU69768 Human pro

# ALIGNMENTS

24	577	76.1	220	4	AAB74806 Prostate
25	577	76.1	220	4	AAAG9008 Human pro
26	577	76.1	220	4	AAAG62147 Human pro
27	577	76.1	220	4	ABU71659 Prostate
28	577	76.1	220	5	ABP54355 Human pro
29	577	76.1	220	6	ABP54355 Human pro
30	577	76.1	220	7	ADG26193 Human pro
31	577	76.1	220	10	AEF66474 Human pro
32	577	76.1	220	4	AAU72526 Human pro
33	577	76.1	226	5	AAU74902 Human pro
34	577	76.1	226	5	AAU74902 Human pro
35	577	76.1	226	5	AAU74902 Human pro
36	577	76.1	231	2	AAU25510 Human pro
37	577	76.1	231	2	AAU25510 Human pro
38	577	76.1	249	3	AAU21307 Human pro
39	577	76.1	253	3	AAU21308 Human pro
40	577	76.1	254	3	AAU21320 Human pro
41	577	76.1	254	3	AAU21294 Human pro
42	577	76.1	254	4	AAU72525 Human pro
43	577	76.1	254	4	AAU01174 Human pro
44	577	76.1	254	4	AAU69819 Human pro
45	577	76.1	254	4	AAU69819 Human pro

RESULT 1  
AAB50449  
ID AAB50449 standard; protein; 146 AA.

AC AAB50449;  
DT 14-MAR-2001 (first entry)

DE Human prostate cancer-related intracellular protein #3.

KW Human; prostate cancer; intracellular protein; cytosolic; gene therapy;  
KW breast cancer.

OS Homo sapiens.

PN MO200071711-A2.

PD 30-NOV-2000.

PF 19-MAY-2000; 2000MO-IB000673.

PR 20-MAY-1999; 99US-0135325P.

PR 20-MAY-1999; 99US-0135333P.

PA (SAAT/) SAATCIOGLU F.

PI Saatioglu F;

DR WPI, 2001-032036/04.

DR N-PSDB; AAC90119; AAC90126.

PT Novel nucleic acids encoding intracellular proteins useful for detecting

PT neoplastic cell in a mammal, preferably the presence of prostate cancer

PT or breast cancer.

PS Claim 27; Page 23-24; 47pp; English.

XX The present sequence is an intracellular protein which is encoded by a  
XX gene that is differentially expressed in neoplastic cells, particularly  
XX prostate cancer cells. The polynucleotides and polypeptides are useful  
XX for diagnosing or detecting prostate cancer and breast cancer cells. The  
XX polynucleotides and polypeptides are also useful for treating cancer by  
XX antitense therapy, and antibody based therapy, respectively. Note; The  
XX present sequence is given as SEQ ID NO: 17 in the sequence listing. SEQ  
XX ID NO: 17 is referred to in claim 27, but is described as an RNA  
XX molecule, rather than as a polypeptide

XX	Sequence 146 AA;
XX	
QY	Query Match            100.0%;   Score 758; DB 4; Length 146;
CC	Best Local Similarity   100.0%;   Pred. No. 1.7e-63;
PT	Matches 146; Conservative   0; Mismatches   0; Indels   0; Gaps   0
Db	
QY	1 MENEILFCSGVLVHPOMWLSAAHCFONSYYTGLGIHLSEADQEPGSGQWEASLSTRHPEYN 60
Db	1 MENELFCSGVLVHPOMWLSAAHCFONSYYTGLGIHLSEADQEPGSGQWEASLSTRHPEYN 60
QY	61 RPLIANDMLMIKDESVESDTRISISIASOCPTAGNSCLVSCWGLLANGELTGVCLEPSS 120
Db	61 RPLIANDMLMIKDESVESDTRISISIASOCPTAGNSCLVSCWGLLANGELTGVCLEPSS 120
QY	121 RRSSAOSRGLTOSASQAECLEPCCSA 146
Db	121 RRSSAOSRGLTOSASQAECLEPCCSA 146
RESULT 2	
ID	ABP54355
AC	ABP54355 standard; protein; 195 AA.
XX	
DT	20-JAN-2003 (first entry)
XX	
DE	Human KIK4 alternatively spliced variant protein SEQ ID NO:2.
XX	
KM	Human; KIK4; cancer; benign tumour; cytostatic; variant.
XX	
SN	Homo sapiens.
PN	MO200277243-A1.
PD	03-OCT-2002.
XX	
PF	27-MAR-2002; 2002WO-AU000378.
XX	
PR	27-MAR-2001; 2001AU-00004022.
PA	(UYOU-) UNIV QUEENSLAND TECHNOLOGY.
PI	Dong Y, Clements JA;
XX	
DR	N-PDB; AB083341.
PT	Detecting the presence or diagnosing the risk of cancer or benign tumor,
XX	e.g. an ovarian, endometrial or prostate cancer, by determining the
PT	presence of or detecting aberrant expression of KIK4 in a biological
XX	sample from the patient.
PS	
XX	
PS	Claim 83; Fig 7; 126pp; English.
XX	
CC	The present invention describes a method (M1) for detecting the presence
CC	or diagnosing the risk of cancer or benign tumour in a patient. M1
CC	comprises determining the presence of or detecting aberrant expression of
CC	KIK4 in a biological sample obtained from the patient. KIK4 has
CC	cytostatic activity. The method is useful for detecting the presence or
CC	diagnosing the risk of a cancer or a benign tumour in a patient,
CC	particularly an ovarian, endometrial or prostate cancer, or a cancer or
CC	benign tumour associated with an organ or tissue used for restoring or
CC	endometrium or prostate. An agent which can be used for restoring or
CC	modulating KIK4 expression can be used for treating or preventing cancer
CC	or benign tumour. KIK4 polynucleotides, polypeptides or antigen-binding
CC	molecules from the present invention can be used for detecting aberrant
CC	KIK4 polynucleotides or aberrant K4 polypeptides that correlate with a
CC	cancer or a benign tumour. The present sequence represents a human KIK4
CC	alternatively spliced variant from the present invention
XX	
XX	
50	Sequence 195 AA;

Query Match	Best Local Similarity	Score	DB 6;	Length	195;
Matches 146;	Conservative	0;	Mismatches	0;	Indels
					Gaps
					0;

  

Query Match	Best Local Similarity	Score	DB 3;	Length	237;
Matches 114;	Conservative	0;	Mismatches	0;	Indels
					Gaps
					0;

OY 1 MENELFCGVLVHPQWVLSAHCFOFNSYITIGLHSLLEADQEPGSGQWEASLSVRHPEYN 60  
 DB 29 MENELFCGVLVHPQWVLSAHCFOFNSYITIGLHSLLEADQEPGSGQWEASLSVRHPEYN 88  
 OY 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG 114  
 DB 89 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG 142

RESULT 4

AAW69389 ID AAW69389 standard; protein; 164 AA.

AAW69389; AC

DT 25-MAR-2003 (revised)

DE Prostate tumour specific gene clone DE14 protein.

XX Prostate tumour specific gene; human; prostate cancer; detection;  
 KM therapy.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 118 /note= "unspecified amino acid"

PN MO9837418-A2.

XX 27-AUG-1998.

PF 25-FEB-1998; 98WO-US003690.

PR 25-FEB-1997; 97US-00806596.

PR 01-AUG-1997; 97US-00904809.

PR 09-FEB-1998; 98US-00020747.

PA (CORI-) CORIXA CORP.

PI Xu J, Dillon DC;

DR WPI; 1998-480805/41.

DR N-PSDB; AAV58648.

XX Novel human prostate specific tumour protein and fragments - useful for  
 PT detecting and treating prostate cancers.

XX Example 1; Page 117-118; 141pp; English.

XX This sequence is encoded by a human prostate tumour specific gene, and  
 CC can be used in the method of the invention. The method is for detecting  
 CC prostate cancer comprising contacting a biological sample with an agent  
 CC able to bind an immunogenic portion of a prostate protein (such as this  
 CC protein sequence). An antibody which binds to an immunogenic portion of  
 CC the prostate protein, and the method can be used to detect, monitor  
 CC progression of, or treat prostate cancers. The antibody may also be  
 CC conjugated to a therapeutic agent for use in therapy of prostate cancers.  
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 164 AA;

Query Match 76.1%; Score 577; DB 2; Length 164;

Best Local Similarity 77.1%; Pred. No. 2.4e-46; Indels 14; Gaps 3;

Matches 118; Conservative 5; Mismatches 16;

OY 1 MENELFCGVLVHPQWVLSAHCFOFNSYITIGLHSLLEADQEPGSGQWEASLSVRHPEYN 60

DB 1 MENELFCGVLVHPQWVLSAHCFOFNSYITIGLHSLLEADQEPGSGQWEASLSVRHPEYN 60

OY 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG----- 115

DB 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG----- 115

DB 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG----- 120  
 OY 116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144  
 DB 121 GWEBC-----EKLSPWGGCTTSATSSAR-TSCC 148

RESULT 5

AAW71873 ID AAW71873 standard; protein; 164 AA.

AAW71873; AC

DT 06-JAN-1999 (first entry)

DE Protein encoded by prostate tumour clone P703 splice variant DE14.

XX Prostate; cancer; tumour; vaccine; immunogen; clone.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 118 /note= "undefined residue"

PN MO9837093-A2.

XX 27-AUG-1998.

PF 25-FEB-1998; 98WO-US003492.

PR 25-FEB-1997; 97US-00806099.

PR 01-AUG-1997; 97US-00904804.

PR 09-FEB-1998; 98US-00020956.

PA (CORI-) CORIXA CORP.

PI Xu J, Dillon DC;

DR WPI; 1998-609886/51.

XX Polypeptides comprising immunogenic portions of prostate proteins - used  
 PT in a vaccine for the treatment of prostate cancer.

XX Example 3; Page 109; 130pp; English.

XX The present sequence is an immunogenic portion of a prostate tumour  
 CC protein. The immunogen, or the DNA encoding it, can be used as a vaccine  
 CC for the treatment of prostate cancer. The immunogen was isolated from a  
 CC prostate tumour cDNA library obtained by subtracting a prostate tumour  
 CC cDNA expression library with a normal tissue cDNA library

XX Sequence 164 AA;

Query Match 76.1%; Score 577; DB 2; Length 164;

Best Local Similarity 77.1%; Pred. No. 2.4e-46; Indels 14; Gaps 3;

Matches 118; Conservative 5; Mismatches 16;

OY 1 MENELFCGVLVHPQWVLSAHCFOFNSYITIGLHSLLEADQEPGSGQWEASLSVRHPEYN 60

DB 1 MENELFCGVLVHPQWVLSAHCFOFNSYITIGLHSLLEADQEPGSGQWEASLSVRHPEYN 60

OY 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG----- 115

DB 61 RPLANDMLIKLDESSESPTIRISISASOCPPTAGNSCLVSGWGLANGELTG----- 115

OY 116 -----CLPSSRRSSAQSRLTQSSASQAECCLPCC 144

DB 121 GWEBC-----EKLSPWGGCTTSATSSAR-TSCC 148

RESULT 6

AAW82006

```
ID AAY82006 standard; protein; 164 AA.
XX
XX AAY82006;
AC
XX
XX 13-JUN-2000 (first entry)
DT
XX
XX Human immunogenic prostate tumour protein sequence SEQ ID NO:178.
DE
XX
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX WO200004149-A2.
PN
XX
XX 27-JAN-2000.
PD
XX
XX 14-JUL-1999; 99WO-US015838.
PE
XX
XX 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 98US-00232149.
PR 15-JAN-1999; 98US-00232860.
PR 09-APR-1999; 99US-00288946.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL,
PI
XX
XX WPI; 2000-171268/15.
DR
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
XX Claim 3; Page 160; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idiotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
CC the present invention
XX
XX Sequence 164 AA;
SQ
Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 2.4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
OY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWEASLSVRHPEYN 60
OY 61 RPLLANDMLIKLDESVESDTRISISTIASQCPAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLLANDMLIKLDESVESDTRISISTIASQCPAGNSCLVSGWGLANGELTGV----- 115
OY 116 -----CLPSSRRSSNQSRGLTQSSASQAELPCC 144
DB 121 GGMWC-----EKLSDPQGGCTTSATSSAR-TSCC 148
```

RESULT 7  
ABG94415

```
ID ABG94415 standard; protein; 164 AA.
XX
XX ABG94415;
AC
XX
XX 27-NOV-2002 (first entry)
DT
XX
XX Human prostate tumour protein partial variant sequence #3.
DE
XX
XX Human; immunogenic; prostate protein; prostate tumour protein;
KW prostate cancer; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX US2002090372-A1.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 14-JUL-1998; 98US-00115453.
PE
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
XX
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
XX
XX Xu J, Dillon DC;
PI
XX
XX WPI; 2000-171268/15.
DR N-PSDB; ABS71316.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
XX Example 3; Page 82; 101pp; English.
XX
XX The present invention relates to a new polypeptide comprising an
CC immunogenic portion of a prostate protein. The invention is useful for
CC inhibiting the development of prostate cancer in a patient. The invention
CC is also useful as markers for diagnosing prostate cancer and for
CC monitoring diseases progression in patients. The present amino acid
CC sequence represents a variant human prostate tumour protein
XX
XX Sequence 164 AA;
SQ
Query Match 76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 2.4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
OY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGSGQWEASLSVRHPEYN 60
OY 61 RPLLANDMLIKLDESVESDTRISISTIASQCPAGNSCLVSGWGLANGELTGV----- 115
DB 61 RPLLANDMLIKLDESVESDTRISISTIASQCPAGNSCLVSGWGLANGELTGV----- 115
OY 116 -----CLPSSRRSSNQSRGLTQSSASQAELPCC 144
DB 121 GGMWC-----EKLSDPQGGCTTSATSSAR-TSCC 148
```

RESULT 8  
AA01121  
ID AA01121 standard; protein; 164 AA.  
XX  
XX AA01121;  
AC  
XX  
XX 04-OCT-2001 (first entry)  
DT  
XX  
XX Human prostate-specific amino acid sequence P703P-DE14.  
DE  
XX

KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
 KW cytostatic; gene therapy; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200151633-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 16-JAN-2001; 2001WO-US001574.  
 XX  
 PR 14-JAN-2000; 2000US-00483672.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
 PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;  
 PI Wang A, Meagher MJ;  
 XX  
 DR WPI; 2001-425873/45.  
 XX  
 PT New polynucleotide encoding a prostate-specific protein, for diagnosing,  
 PT monitoring and treating prostate cancer in a patient and for use in  
 PT vaccines.  
 PT  
 PS Claim 2; Page 288; 543pp; English.  
 XX  
 XX The present invention describes polynucleotide sequences (I) which encode  
 CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
 CC and can be used in vaccine production and gene therapy. (I), (II), T cells  
 CC antibodies to (II), fusion proteins comprising (II), and isolated T cells  
 CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and  
 CC the antibodies are also used in the detection of cancer in a patient. The  
 CC cancer that is diagnosed or treated is particularly prostate cancer. (I)  
 CC and (II) can be used in vaccines. The antibodies or (I) can be used for  
 CC monitoring the progression of cancer in a patient. (I) and (II) can also  
 CC be used to improve diagnostic and therapeutic methods for prostate  
 CC cancer. They can indicate the level of metastasis as well as the prostate  
 CC volume. AAH93357 to AAH93944 and AA01115 to AA01318 represent  
 CC polynucleotide and amino acid sequences used in the exemplification of  
 CC the present invention  
 CC  
 SQ Sequence 164 AA;  
 XX  
 Query Match 76.1%; Score 577; DB 4; Length 164;  
 Best Local Similarity 77.1%; Pred. No. 2,4e-46;  
 Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;  
 OY 1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGHSLEADQEGSQWVEASLSVRHEYN 60  
 Db 1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGHSLEADQEGSQWVEASLSVRHEYN 60  
 OY 61 RPLANDLMIKLDESSESDTIRISISASQCTAGNSCLVSGMGLANGELTGV----- 115  
 Db 61 RPLANDLMIKLDESSESDTIRISISASQCTAGNSCLVSGMGLANGELTGV----- 115  
 OY 116 -----CLPSSRRSSAOSRGLTOSASQAECPLCC 144  
 Db 121 GWEC-----EKLSPWOGCTISATSSAR-TSCC 148  
 Db  
 RESULT 9  
 AAU69767  
 ID AAU69767 standard; protein; 164 AA.  
 XX  
 AC AAU69767;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE Human prostate cDNA encoded protein #7.  
 XX  
 KW Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200173032-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009919.  
 XX  
 PR 27-MAR-2000; 2000US-00536857.  
 XX  
 PR 09-MAY-2000; 2000US-00568100.  
 XX  
 PR 12-MAY-2000; 2000US-00570737.  
 XX  
 PR 13-JUN-2000; 2000US-00593793.  
 XX  
 PR 27-JUN-2000; 2000US-00605783.  
 XX  
 PR 09-AUG-2000; 2000US-00636215.  
 XX  
 PR 29-AUG-2000; 2000US-00651236.  
 XX  
 PR 06-SEP-2000; 2000US-00657279.  
 XX  
 PR 02-OCT-2000; 2000US-00679426.  
 XX  
 PR 10-OCT-2000; 2000US-00685166.  
 XX  
 PR 09-NOV-2000; 2000US-00709729.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carter D;  
 PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;  
 XX  
 DR WPI; 2001-639232/73.  
 XX  
 DR N-PSDB; AAS63619.  
 XX  
 PT New human prostate-specific polypeptides and polynucleotides useful for  
 PT the diagnosis and treatment of cancer, especially prostate cancer.  
 PT  
 PS Claim 2; Page 290; 579pp; English.  
 XX  
 XX The invention relates to isolated prostate-specific polynucleotides,  
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised  
 CC against the polypeptides (or antigenic epitopes derived from them) and  
 CC antigen-presenting cells expressing the polypeptides. The antibodies are  
 CC useful for detecting the presence of cancer, especially prostate cancer.  
 CC The polypeptides, polynucleotides and the antigen-presenting cells are  
 CC useful for stimulating and/or expanding T cells specific for a tumour  
 CC protein, and for inhibiting the development of cancer especially prostate  
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are  
 CC useful for stimulating an immune response, and for treating cancer. The  
 CC oligonucleotide is useful for detecting cancer. The present sequence is a  
 CC prostate specific polypeptide of the invention  
 CC  
 SQ Sequence 164 AA;  
 XX  
 Query Match 76.1%; Score 577; DB 4; Length 164;  
 Best Local Similarity 77.1%; Pred. No. 2,4e-46;  
 Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;  
 OY 1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGHSLEADQEGSQWVEASLSVRHEYN 60  
 Db 1 MENELFCGVLVHPQWVLSAHCFOFNSYITGLGHSLEADQEGSQWVEASLSVRHEYN 60  
 OY 61 RPLANDLMIKLDESSESDTIRISISASQCTAGNSCLVSGMGLANGELTGV----- 115  
 Db 61 RPLANDLMIKLDESSESDTIRISISASQCTAGNSCLVSGMGLANGELTGV----- 115  
 OY 116 -----CLPSSRRSSAOSRGLTOSASQAECPLCC 144  
 Db 121 GWEC-----EKLSPWOGCTISATSSAR-TSCC 148  
 Db  
 RESULT 10  
 AAB74804  
 ID AAB74804 standard; protein; 164 AA.  
 XX  
 AC AAB74804;  
 XX  
 DT 14-JUN-2001 (first entry)  
 XX

XX Prostate tumour antigen predicted amino acid sequence for P703P-DE14.  
DE  
XX  
XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;  
KW prostate cancer; immunogenic; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO200125272-A2.  
XX  
XX 12-APR-2001.  
XX  
PD 04-OCT-2000; 2000WO-US027464.  
XX  
PF 04-OCT-1999; 99US-0157455P.  
XX  
PR 04-OCT-1999; 99US-0157455P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Skeiky YAM, Reed SG, Cheever MA;  
XX  
XX WPI; 2001-245062/25.  
XX  
DR N-PSDB; AAH02592.  
XX  
PT Prostate specific protein and its encoding polynucleotide, useful for the  
PT treatment and diagnosis of prostate cancer.  
XX  
PS Claim 3; Page 177; 276pp; English.  
XX  
CC The present invention describes an isolated polypeptide (I) comprising at  
CC least an immunogenic portion of a prostate tumor antigen protein or its  
CC variant. (I) have cytostatic activity and can be used in vaccine  
CC production. (I), prostate tumour antigen polynucleotides, an antigen  
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a  
CC pharmaceutical composition containing (I) are useful for inhibiting the  
CC development of cancer in a patient. Antibodies specific for prostate  
CC specific proteins and oligonucleotides that hybridise to a polynucleotide  
CC that encodes a prostate specific protein are useful for detecting the  
CC presence or absence of a cancer or monitoring the progression of the  
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,  
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the  
CC exemplification of the present invention  
XX  
XX Sequence 164 AA;  
SQ

Query Match 76.1%; Score 577; DB 4; Length 164;  
Best Local Similarity 77.1%; Pred. No. 2,4e-46;  
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHSLADQEPGQWVEASLSVRHPEYN 60  
DB 1 MENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHSLADQEPGQWVEASLSVRHPEYN 60  
QY 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115  
DB 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115  
QY 116 ----CLPSSRRSSAOSRGLTOSASQAECPLCC 144  
DB 121 GWMEC----EKLSPWQGGCTISATSSAR-TSCC 148

RESULT 11  
AAG99006  
ID AAG99006 standard; protein; 164 AA.  
XX  
AC AAG99006;  
XX  
DT 25-SEP-2001 (first entry)  
XX  
DE Human prostate-specific amino acid sequence P703P-DE14.  
XX  
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;  
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;

KW prostate specific antigen; PSA.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200134802-A2.  
XX  
XX 17-MAY-2001.  
XX  
PD 09-NOV-2000; 2000WO-US030904.  
XX  
PF 12-NOV-1999; 99US-00439313.  
XX  
PR 18-NOV-1999; 99US-00443686.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;  
XX  
XX WPI; 2001-308785/32.  
XX  
PT Isolated polypeptide comprising at least an immunogenic portion of a  
PT prostate-specific protein, useful in the diagnosis and therapy of  
PT prostate cancer.  
XX  
PS Claim 3; Page 188; 325pp; English.  
XX  
CC The present invention describes an isolated polypeptide (P1) comprising  
CC at least an immunogenic portion of a prostate-specific protein, or its  
CC variant. Also described are polynucleotides (N1) encoding (P1) and  
CC (N1) have cytostatic activity and can be used in vaccine production. The  
CC polypeptides, nucleic acids and antibodies from the present invention are  
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific  
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic  
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.  
CC Prostate specific antigen (PSA) P5015 was located on chromosome 1.  
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide  
CC and polypeptide sequences used in the exemplification of the present  
CC invention  
XX  
XX Sequence 164 AA;  
SQ

Query Match 76.1%; Score 577; DB 4; Length 164;  
Best Local Similarity 77.1%; Pred. No. 2,4e-46;  
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHSLADQEPGQWVEASLSVRHPEYN 60  
DB 1 MENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHSLADQEPGQWVEASLSVRHPEYN 60  
QY 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115  
DB 61 RPLLANDMLIKLDESVESDTRISISIASOCPAGNSCLVSGWGLANGELTGV----- 115  
QY 116 ----CLPSSRRSSAOSRGLTOSASQAECPLCC 144  
DB 121 GWMEC----EKLSPWQGGCTISATSSAR-TSCC 148

RESULT 12  
ABU71657  
ID ABU71657 standard; protein; 164 AA.  
XX  
AC ABU71657;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Prostate cancer specific antigen P703P #3.  
XX  
KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;  
KW immunogen; cancer; prostate specific antigen.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX	US2002192763-A1.
XX	
PD	19-DEC-2002.
XX	
PF	29-JUN-2001; 2001US-00895793.
XX	
XX	04-OCT-1999; 99US-0157455P.
PR	04-OCT-2000; 2000US-00679272.
PR	28-MAR-2001; 2001US-00822827.
XX	
XX	(XUJU/) XU J.
PA	(DILL/) DILLON D C.
PA	(MITC/) MITCHAM J L.
PA	(HARL/) HARLOCKER S L.
PA	(JIAN/) JIANG Y.
PA	(KALO/) KALOS M D.
PA	(FANG/) FANGER G R.
PA	(RETT/) RETTER M W.
PA	(STOL/) STOLK J A.
PA	(DAYC/) DAY C H.
PA	(VEDV/) VEDVICK T S.
PA	(CART/) CARTER D.
PA	(LISX/) LI S X.
PA	(WANG/) WANG A.
PA	(SKEI/) SKEIKY Y A W.
PA	(HEPL/) HEPLER W T.
PA	(HENR/) HENDERSON R A.
PA	(HURA/) HURAL J.
PA	(MCNE/) MCNELL P D.
PA	(HOUG/) HOUGHTON R L.
PA	(DBAS/) Y DE BASSOLS C V.
PA	(FOYT/) FOY T M.
XX	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI	Mcnell PD, Houghton RL, Y De BassolsCV, Foy TM;
DR	WPI; 2001-245062/25.
PT	Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
XX	
PS	Example 3; SEQ ID NO 178; 85bp; English.
CC	The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 3 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This is the amino acid sequence of a prostate cancer specific antigen. Notes: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?docID=US20020192763
SO	Sequence 164 AA:
Oy	Query Match 76.1%; Score 577; DB 4; Length 164; Best Local Similarity 77.1%; Pred. No. 2, 4e-46; Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3
Dd	1 MENELFCGCVLVHPQWVLGAHCFOHSYITGLGLSHLEADDEPGSGOMVEASLSVRHPEYN 60 1 MENELFCGCVLVHPQWVLGAHCFOHSYITGLGLSHLEADDEPGSGOMVEASLSVRHPEYN 60
Oy	61 RPULANDMLILKLDESVSSEDTFRISISIOCPFAANSCLVSGMGLANGELTGV----- 115 61 RPULANDMLILKLDESVSSEDTFRISISIOCPFAANSCLVSGMGLANGELTGV----- 115
Dd	61 RPULANDMLILKLDESVSSEDTFRISISIOCPFAANSCLVSGMGLANGELTGV----- 115 61 RPULANDMLILKLDESVSSEDTFRISISIOCPFAANSCLVSGMGLANGELTGV----- 115

```

YY      116 -----CLPSSRRSSAQSRLTQSSASQAECPLPCG 144
XX      |         :         :         :         :         :         :         :         :         :         :
DB      121 GGMWEC----EKLSQPWGCGCTTSATSSAR-TSCC 148

RESULT 13
AAU04965
ID   AAU04965 standard; protein; 164 AA.
XX
XX
AC   AAU04965;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human prostate tumour protein DE14.
XX
KW   Human; prostate tumour protein; prostate cancer.
XX
OS   Homo sapiens.
XX
PN   US6262245-B1.
XX
PD   17-JUL-2001.
XX
PF   25-FEB-1998;    98US-00030607.
XX
PR   25-FEB-1997;    97US-00860609.
PR   01-AUG-1997;    97US-00904804.
PR   09-FEB-1998;    98US-00020956.
XX
PA   (CORI-) CORIXA CORP.
PI   Xu J, Dillon DC;
XX
DR   WPI, 2001-440862/47.
DR   N-PSDB; AAS10170.
XX
PT   Novel polynucleotide encoding polypeptide comprising a portion of
PT   prostate tumor protein useful for inhibiting development of prostate
PT   cancer or for treating prostate cancer in a patient.
XX
PS   Example 2; Col 176-177; 105pp; English.
XX
CC   The sequence is a partial prostate tumour protein, encoded by a prostate
CC   tumour specific cDNA. The DNA is useful for inhibiting the development of
CC   prostate cancer or for treating prostate cancer in a patient
XX
SQ   Sequence 164 AA;
Query Match          76.1%; Score 577; DB 4; Length 164;
Best Local Similarity 77.1%; Pred. No. 2,4e-46;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3

YY      1 MENELFCSGVLAHPQWVLAAACFPONSVTIGLGLHLEADDPGSQWYEASTSVHPPEYN 60
XX      |||||
DB      1 MENELFCSGVLAHPQWVLAAACFPONSVTIGLGLHLEADDPGSQWYEASTSVHPPEYN 60
YY      61 RPLLANDMLILKIDSVSRSDFTRISIASQCPTAGNSCLVSGWGLANGELTV----- 115
XX      |||||
DB      61 RPLLANDMLILKIDSVSRSDFTRISIASQCPTAGNSCLVSGWGLANDAVIAIAIOSXTV 120
YY      116 ----CLPSSRRSSAQSRLTQSSASQAECPLPCG 144
XX      |         :         :         :         :         :         :         :         :         :         :
DB      121 GGMWEC----EKLSQPWGCGCTTSATSSAR-TSCC 148

RESULT 14
ABB95226
ID   ABB95226 standard; protein; 164 AA.
XX
AC   ABB95226;
XX
DT   19-JUL-2002 (first entry)

```



XX DE Human P703P-DE14 protein SEQ ID NO 178.  
XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;  
XX KW gene therapy.  
XX OS Homo sapiens.  
XX PN US2002022248-A1.  
XX PD 21-FEB-2002.  
XX PF 12-JAN-2001; 2001US-00759143.  
XX PR 25-FEB-1997; 97US-00806099.  
XX PR 01-AUG-1997; 97US-00904804.  
XX PR 10-FEB-1998; 98US-00020956.  
XX PR 25-FEB-1998; 98US-00030607.  
XX PR 14-JUL-1998; 98US-00115453.  
XX PR 23-SEP-1998; 98US-00159812.  
XX PR 15-JAN-1999; 99US-00232149.  
XX PR 09-APR-1999; 99US-00288946.  
XX PR 13-JUL-1999; 99US-00352616.  
XX PR 12-NOV-1999; 99US-00439313.  
XX PR 18-NOV-1999; 99US-00433686.  
XX PR 14-JAN-2000; 2000US-00483672.  
XX PR 27-MAR-2000; 2000US-00536857.  
XX PR 09-MAY-2000; 2000US-00568100.  
XX PR 12-MAY-2000; 2000US-00570737.  
XX PR 13-JUN-2000; 2000US-00593793.  
XX PR 27-JUN-2000; 2000US-00605783.  
XX PR 10-AUG-2000; 2000US-00636215.  
XX PR 29-AUG-2000; 2000US-00651216.  
XX PR 06-SEP-2000; 2000US-00657279.  
XX PR 02-OCT-2000; 2000US-00679426.  
XX PR 10-OCT-2000; 2000US-00685166.  
XX PA (XUUU/) XU J.  
XX PA (DILL/) DILLON D C.  
XX PA (MITC/) MITCHAM J L.  
XX PA (HARL/) HARLOCKER S L.  
XX PA (JIANG/) JIANG Y.  
XX PA (KALO/) KALOS M D.  
XX PA (FRANG/) FRANGER G R.  
XX PA (RETT/) RETTER M W.  
XX PA (STOL/) STOLK J A.  
XX PA (DAYC/) DAY C H.  
XX PA (VEDV/) VEDVICK T S.  
XX PA (CART/) CARTER D.  
XX PA (LISX/) LI S X.  
XX PA (WANG/) WANG A.  
XX PA (SKEI/) SKEIKY Y A W.  
XX PA (HEPL/) HEPLER W T.  
XX PA (HEND/) HENDERSON R A.  
XX PT Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,  
XX PT Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;  
XX PT Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
XX DR WPI; 2002-255649/30.  
XX PT New prostate-specific polynucleotides for diagnosing and treating  
XX PT diseases, in particular prostate cancer, and as markers for the  
XX PT progression of cancer.  
XX PS Claim 2; SEQ ID NO 178; 87bp; English.  
XX CC The present invention provides prostate-specific coding sequences and  
XX CC their encoded proteins. These can be used in the diagnosis and treatment  
XX CC of cancers, particularly prostate cancer. The present sequence is a  
XX CC protein described in the invention  
XX SO Sequence 164 AA;

Query Match 76.1%; Score 577; DB 5; Length 164;  
Best Local Similarity 77.1%; Pred. No. 2,4e-46;  
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;  
QY 1 MENELFCGVLVHPQWVLSAHCDFONSYYTGLGLHSLEAOEPGSOVSEASLVRHPEYN 60  
DB 1 MENELFCGVLVHPQWVLSAHCDFONSYYTGLGLHSLEAOEPGSOVSEASLVRHPEYN 60  
QY 61 RPLANDLMIKLDSESVESDITRISISIASQCPAGNSCLVSGWGLHANGELTGV----- 115  
DB 61 RPLANDLMIKLDSESVESDITRISISIASQCPAGNSCLVSGWGLHANGELTGV----- 115  
QY 116 ---CLPSSRRSSAQSRLTQSSAQAECPLCC 144  
DB 121 GWEC---EKLSPWOGCTTISATSSAR-TSCC 148  
RESULT 15  
ABG76669  
ID ABG76669 standard; protein; 164 AA.  
XX AC ABG76669;  
XX DT 05-NOV-2002 (first entry)  
XX DE Prostate tumour protein #7.  
XX KW Human; prostate tumour; immunotherapy; prostate cancer.  
XX OS Homo sapiens.  
XX PN US2002081580-A1.  
XX PD 27-JUN-2002.  
XX PR 25-FEB-1998; 98US-00030606.  
XX PR 25-FEB-1997; 97US-00806596.  
XX PR 01-AUG-1997; 97US-00904809.  
XX PR 09-FEB-1998; 98US-00020747.  
XX PA (XUUU/) XU J.  
XX PA (DILL/) DILLON D C.  
XX PI Xu J, Dillon DC;  
XX DR WPI; 2002-607662/65.  
XX PT Detecting prostate cancer comprises contacting a sample with an agent  
XX PT capable of binding to a polypeptide with an immunogenic portion of a  
XX PT prostate protein, oligonucleotide primers or a probe specific for DNA  
XX PT encoding the polypeptide.  
XX PS Claim 1; Page 92; 11pp; English.  
XX CC The invention relates to a method of detecting prostate cancer by  
XX CC contacting a biological sample from a patient with: (a) a binding agent  
XX CC that binds to a polypeptide having an immunogenic portion of a prostate  
XX CC protein or its variant; (b) 2 oligonucleotide primers, where 1 of the  
XX CC oligonucleotides is specific for a DNA encoding the polypeptide of (a);  
XX CC or (c) an oligonucleotide probe specific for a DNA molecule encoding the  
XX CC polypeptide of (a). The method and polypeptides are useful for  
XX CC diagnosing, treating, particularly by immunotherapy, monitoring the  
XX CC progression, and inhibiting the development of prostate cancer in a  
XX CC patient. The polypeptides may be used to generate antibodies useful for  
XX CC the diagnosis and monitoring of prostate cancer. ABG76663-ABG76669  
XX CC represent human prostate tumour protein sequences of the invention  
XX SO Sequence 164 AA;  
Query Match 76.1%; Score 577; DB 5; Length 164;  
Best Local Similarity 77.1%; Pred. No. 2,4e-46;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3,

```

OY      1  MENELFCGCVLVHPOMWTLAAACHFONSXYTIGLGLSLNADQEGSQMWVASLSVRRPEYN  60
        |||||
Db      1  MENELFCGCVLVHPOMWTLAAACHFONSXYTIGLGLSLNADQEGSQMWVASLSVRRPEYN  60
        |||||

OY      61  RPLANDMLILKLDSEVSSEDTRIISIAOCPETAGNSCLVSGWGLLNGELTGV-----  115
        |||||
Db      61  RPLANDMLILKLDSEVSSEDTRIISIAOCPETAGNSCLVSGWGLLNDVIAIGSXTV  120
        |||||

OY      116  ---CLPSSRRSSAQRGLTQSSASQAECPLCC  144
        ||| : |||
Db      121  GSWEC-----EKLSQPMWGCTTISATSGAR-TSCC  148
        ||| : |||

```

Search completed: August 29, 2006, 03:41:57  
Job time : 199 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd

OM protein - protein search, using sw model

Run on: August 29, 2006, 03:59:14 ; Search time 176 Seconds  
(without alignments)  
384.258 Million cell updates/sec

Title:	US-10-726-093-10
Perfect score:	758
Sequence:	1 MENEELFCSGVLVHPQWVLSA.....SRGLTQSASQAELPCCSA 146

Scoring table: BLOSUM62

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : Published.Applications.Ala.Matin:*
1: /EMC_Celerra_SIDS3/pdata/2/pubpaa/US07_PUBCOMB.pcp:*
2: /EMC_Celerra_SIDS3/pdata/2/pubpaa/US08_PUBCOMB.pcp:*
3: /EMC_Celerra_SIDS3/pdata/2/pubpaa/US09_PUBCOMB.pcp:*
4: /EMC_Celerra_SIDS3/pdata/2/pubpaa/US10A_PUBCOMB.pcp:*
5: /EMC_Celerra_SIDS3/pdata/2/pubpaa/US10B_PUBCOMB.pcp:*
6: /EMC_Celerra_SIDS3/pdata/2/pubpaa/US11_PUBCOMB.pcp:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	758	100.0	146	5	US-10-726-093-10	Sequence 10, Appl1
2	758	100.0	195	4	US-10-473-485-2	Sequence 2, Appl1
3	577	76.1	164	3	US-09-759-143-178	Sequence 178, App
4	577	76.1	164	3	US-09-780-669-178	Sequence 178, App
5	577	76.1	164	3	US-09-822-827-178	Sequence 178, App
6	577	76.1	164	3	US-09-822-827-178	Sequence 178, App
7	577	76.1	164	3	US-09-115-453-178	Sequence 178, App
8	577	76.1	164	3	US-09-232-880-178	Sequence 178, App
9	577	76.1	164	3	US-09-895-793-178	Sequence 178, App
10	577	76.1	164	3	US-09-895-814-178	Sequence 178, App
11	577	76.1	164	4	US-10-012-896-178	Sequence 178, App
12	577	76.1	164	4	US-10-010-940-178	Sequence 178, App
13	577	76.1	164	4	US-10-144-678A-178	Sequence 178, App
14	577	76.1	164	4	US-10-294-025-178	Sequence 178, App
15	577	76.1	164	4	US-10-688-838-178	Sequence 178, App
16	577	76.1	164	6	US-11-234-786-178	Sequence 178, App
17	577	76.1	205	5	US-10-726-093-8	Sequence 8, Appl1
18	577	76.1	220	3	US-09-759-143-327	Sequence 327, App
19	577	76.1	220	3	US-09-780-669-327	Sequence 327, App
20	577	76.1	220	3	US-09-822-827-327	Sequence 327, App
21	577	76.1	220	3	US-09-822-880-327	Sequence 327, App
22	577	76.1	220	3	US-09-895-793-327	Sequence 327, App
23	577	76.1	220	3	US-09-895-814-327	Sequence 327, App
24	577	76.1	220	4	US-10-012-896-327	Sequence 327, App
25	577	76.1	220	4	US-10-010-940-327	Sequence 327, App
26	577	76.1	220	4	US-10-144-678A-327	Sequence 327, App
27	577	76.1	220	4	US-10-294-025-327	Sequence 327, App

## ALIGNMENTS

4	577	76.1	220	6	US-11-234-786-127	Sequence 327, App
5	577	76.1	226	4	US-10-313-089-8	Sequence 8, Appl
29	577	76.1	254	3	US-09-755-113-525	Sequence 525, App
30	577	76.1	254	3	US-09-780-669-825	Sequence 525, App
31	577	76.1	254	3	US-09-822-827-825	Sequence 525, App
32	577	76.1	254	3	US-09-856-793-525	Sequence 525, App
33	577	76.1	254	3	US-09-859-814-525	Sequence 525, App
34	577	76.1	254	3	US-10-011-896-525	Sequence 525, App
35	577	76.1	254	4	US-10-010-940-525	Sequence 525, App
36	577	76.1	254	4	US-10-312-089-7	Sequence 7, Appl
37	577	76.1	254	4	US-10-144-678A-525	Sequence 525, App
38	577	76.1	254	4	US-10-292-025-525	Sequence 525, App
39	577	76.1	254	4	US-10-473-485-6	Sequence 6, Appl
40	577	76.1	254	4	US-10-473-485-6	Sequence 6, Appl
41	577	76.1	254	4	US-10-473-485-3	Sequence 13, App
42	577	76.1	254	6	US-11-234-786-525	Sequence 525, App
43	577	76.1	284	5	US-10-015-989A-54	Sequence 54, Appl
44	577	76.1	312	4	US-10-313-089-3	Sequence 3, Appl
45	577	76.1	344	3	US-09-822-827-973	Sequence 973, App

```

RESULT 1
US-10-726-093-10
; Sequence 10, Application US/10726093
; Publication No. US20050106643A1
; GENERAL INFORMATION:
; APPLICANT: Satciloglu, Fahri
; TITLE OF INVENTION: Differentially Expressed Genes in
; FILE REFERENCE: 50218/002003
; CURRENT APPLICATION NUMBER: US/10/726,093
; PRIOR APPLICATION NUMBER: US/09/743,682
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/IB00/00673
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/135,325
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 60/135,333
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-093-10

Query Match      100.0%; Score 758; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 1,3e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db      1 MENELFCSGVILHPQWILSAAHCFQNSYTTIGLGLHSLEADDEPGSQMVEASLSVHPEYN 60
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MENELFCSGVILHPQWILSAAHCFQNSYTTIGLGLHSLEADDEPGSQMVEASLSVHPEYN 60

Qy      61 RPLANDMLIKIDESVESPTTISISTASOCPTRAGNCLVSGMGLANGETGVCLPSS 120
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 RPLANDMLIKIDESVESPTTISISTASOCPTRAGNCLVSGMGLANGETGVCLPSS 120

Db      61 RPLANDMLIKIDESVESPTTISISTASOCPTRAGNCLVSGMGLANGETGVCLPSS 120
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 RPLANDMLIKIDESVESPTTISISTASOCPTRAGNCLVSGMGLANGETGVCLPSS 120

Qy      121 RSSAQSRGILTQSASQAECPCCSA 146
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 RSSAQSRGILTQSASQAECPCCSA 146

Db      121 RSSAQSRGILTQSASQAECPCCSA 146
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 RSSAQSRGILTQSASQAECPCCSA 146

RESULT 2
US-10-473-485-2
; Sequence 2, Application US/10473485
; Publication No. US20040137455A1
; GENERAL INFORMATION:
; APPLICANT: Clements, Judith A

```

```
APPLICANT: Dong, Ying
TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign
FILE REFERENCE: DAVI172.004APC
CURRENT APPLICATION NUMBER: US/10/473,485
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: AU PR4022/01
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 195
TYPE: PRT
ORGANISM: human
US-10-473-485-2
```

```
Query Match      100.0%; Score 758; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.9e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGQWVEASLSVRHPEYN 60
DB 50 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGQWVEASLSVRHPEYN 109
QY 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLLANGELTGVCLPSS 120
DB 110 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLLANGELTGVCLPSS 169
QY 121 RRSSAQRGLTQSSASQAECPLPCCA 146
DB 170 RRSSAQRGLTQSSASQAECPLPCCA 195
```

## RESULT 3

```
US-09-759-143-178
Sequence 178, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-759-143-178
```

```
Query Match      76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
```

```
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGQWVEASLSVRHPEYN 60
QY 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLLANGELTGV----- 115
DB 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLLANGELTGV----- 120
QY 116 ---CLPSSRRSSAQRGLTQSSASQAECPLPCC 144
DB 121 GSWEC---EKLSQPWGCTTISATSSAR-TSCC 148
```

## RESULT 4

```
US-09-780-669-178
Sequence 178, Application US/09780669
Patent No. US2002005197A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-780-669-178
```

```
Query Match      76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
```

```
QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGQWVEASLSVRHPEYN 60
QY 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLLANGELTGV----- 115
DB 61 RPLANDMLIKLDESVESEDTRISISASOCPFAGNSCLVSGWGLLANGELTGV----- 120
QY 116 ---CLPSSRRSSAQRGLTQSSASQAECPLPCC 144
DB 121 GSWEC---EKLSQPWGCTTISATSSAR-TSCC 148
```

## RESULT 5

US-09-030-606-178  
Sequence 178, Application US/09030606  
Patent No. US20020081580A1

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030.606  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:

## ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.428C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

## INFORMATION FOR SEQ ID NO: 178:

SEQUENCE CHARACTERISTICS:  
LENGTH: 164 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

US-09-030-606-178

Query Match 76.1%; Score 577; DB 3; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGSGMVEASLSVRHPEYN 60  
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGSGMVEASLSVRHPEYN 60

QY 61 RPLANDMLIKLDESSESPTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115  
DB 61 RPLANDMLIKLDESSESPTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115

QY 116 ----CLPSSRRSSAOSRGLTQSSAQAECPLCC 144  
DB 121 GCGWEC----EKLSQPMQGCITISATSSAR-TSCC 148

## RESULT 6

US-09-822-827-178  
Sequence 178, Application US/09822827  
Patent No. US20020081680A1

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.534C1  
CURRENT APPLICATION NUMBER: US/09/822.827  
CURRENT FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 178  
LENGTH: 164

TYPE: PRP  
ORGANISM: Homo sapien

FEATURE:  
NAME/KEY: VARIANT

LOCATION: (1)...(164)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-822-827-178

Query Match 76.1%; Score 577; DB 3; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGSGMVEASLSVRHPEYN 60  
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGSGMVEASLSVRHPEYN 60

QY 61 RPLANDMLIKLDESSESPTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115  
DB 61 RPLANDMLIKLDESSESPTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115

QY 116 ----CLPSSRRSSAOSRGLTQSSAQAECPLCC 144  
DB 121 GCGWEC----EKLSQPMQGCITISATSSAR-TSCC 148

## RESULT 7

US-09-115-453-178  
Sequence 178, Application US/09115453B  
Patent No. US20020090372A1

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
FILE REFERENCE: 210121.427C4  
CURRENT APPLICATION NUMBER: US/09/115.453B  
CURRENT FILING DATE: 1998-07-14  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 178  
LENGTH: 164

TYPE: PRP

ORGANISM: Homo sapien

FEATURE:  
NAME/KEY: VARIANT

LOCATION: (1)...(164)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-115-453-178

Query Match 76.1%; Score 577; DB 3; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGSGMVEASLSVRHPEYN 60  
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADQEPGSGMVEASLSVRHPEYN 60

QY 61 RPLANDMLIKLDESSESPTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115  
DB 61 RPLANDMLIKLDESSESPTIRISIASOCPAGNSCLVSGMGLANGELTGV----- 115

QY 116 ----CLPSSRRSSAOSRGLTQSSAQAECPLCC 144  
DB 121 GCGWEC----EKLSQPMQGCITISATSSAR-TSCC 148

## RESULT 8

US-09-232-880-178  
Sequence 178, Application US/09232880  
Publication No. US20020182596A1

```

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 178
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(164)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-232-880-178

Query Match          76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

OY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
OY 61 RPLANDMLIKLDSVSESDTIRISISAOCPAGNSCLVSGMGLANGELTGV----- 115
DB 61 RPLANDMLIKLDSVSESDTIRISISAOCPAGNSCLVSGMGLANGELTGV----- 120
OY 116 -----CLPSSRRSSAQSRGLTQSSASQAECCLPCC 144
DB 121 GGMWEC-----EKLSPWQGCITISATSSAR-TSCC 148

RESULT 9
US-09-895-793-178
; Sequence 178, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 178
```

```

; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(164)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-895-793-178

Query Match          76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

OY 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
OY 61 RPLANDMLIKLDSVSESDTIRISISAOCPAGNSCLVSGMGLANGELTGV----- 115
DB 61 RPLANDMLIKLDSVSESDTIRISISAOCPAGNSCLVSGMGLANGELTGV----- 120
OY 116 -----CLPSSRRSSAQSRGLTQSSASQAECCLPCC 144
DB 121 GGMWEC-----EKLSPWQGCITISATSSAR-TSCC 148

RESULT 10
US-09-895-814-178
; Sequence 178, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 178
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(164)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-895-814-178

Query Match          76.1%; Score 577; DB 3; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;
```

```

QY 1 MENTLFCGVLVHPOWYLSAAHCFONSTTIGLGHSLLEADQEPSSQWVSLSVRHPEN 60
    |||||
Db 1 MENTLFCGVLVHPOWYLSAAHCFONSTTIGLGHSLLEADQEPSSQWVSLSVRHPEN 60
    |||||
QY 61 RPLLANDMLTKLPBESVESDTRISISASOCPFAGNSCLVSGMGLLANGEITGV----- 115
    |||||
Db 61 RPLLANDMLTKLPBESVESDTRISISASOCPFAGNSCLVSGMGLLANGEITGV----- 115
    |||||
QY 116 -----CLPSSRRSSAOSRGLTQSSASQAECLPCC 144
    |||||
Db 121 GWMEC-----EKLSDQPMQGCITISATSSAR-TSCC 148
    |||||

```

```

RESULT 11
US-10-012-896-178
: Sequence 178, Application US/10012896
: Publication No. US20020183251A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Jasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Mantanabe, Yoshihiro
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/012,896
: CURRENT FILING DATE: 2001-12-10
: NUMBER OF SEQ ID NOS: 1011
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 178
: LENGTH: 164
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: 118
: OTHER INFORMATION: Xaa = Any Amino Acid
US-10-012-896-178

Query Match 76.1%; Score 577; DB 4; Length 164;
Best Local Similarity 77.1%; Pred. No. 1e-54;
Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3

QY 1 MENELFCGCVLVHPQWVLSAHCQFNSYITGLGLSLHLEADQEPGQOMWEASLSVHPPEYN 60
Db 1 MENELFCGCVLVHPQWVLSAHCQFNSYITGLGLSLHLEADQEPGQOMWEASLSVHPPEYN 60
QY 61 RLPLANDLMLIKIDESVSESDTTRISISIASQCPFAGNSCLVSGWGLLANGELTV----- 115
Db 61 RLPLANDLMLIKIDESVSESDTTRISISIASQCPFAGNSCLVSGWGLLANGELTV----- 115
QY 116 -----CLPSSRRSSAQSRLGTSSASQAELCPCC 144

```

```

      | : | : | |
121 GWEC----EKLSQPWQCTISATSSAR-TSCC 148
Db

```

```

RESULT 12
US-10-010-940-178
Sequence 178, Application US/10010940
Publication No. US2003008062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davyn C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solik, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42793
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ. ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 178
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(164)
OTHER INFORMATION: xaa = Any Amino Acid
US-10-010-940-178

```

[illegible]

US-10-144-678A-178  
 / Sequence 178, Application US/10144678A  
 / Publication No. US930030157089A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Xu, Jiangchun  
 / APPLICANT: Dillon, Davin C.  
 / APPLICANT: Maticham, Jennifer L.  
 / APPLICANT: Harlocker, Susan L.  
 / APPLICANT: Jiang, Yugu  
 / APPLICANT: Henderson, Robert A.  
 / APPLICANT: Kalos, Michael D.  
 / APPLICANT: Fanger, Gary R.  
 / APPLICANT: Retter, Marc W.  
 / APPLICANT: Stolk, John A.  
 / APPLICANT: Day, Craig H.  
 / APPLICANT: Vedvick, Thomas S.  
 / APPLICANT: Carter, David  
 / APPLICANT: Li, Samuel X.



```

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Macanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144, 678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 178
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 118
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-144-678A-178

```

Query Match 76.1%; Score 577; DB 4; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

```

Qy 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQWVEASLSVRHPEYN 60
; 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQWVEASLSVRHPEYN 60
Db 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPTAGNSCLVSGWGLLNDVAVIAIOSXTV 120
; 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPTAGNSCLVSGWGLLNDVAVIAIOSXTV 120
Qy 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
; 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148
Db 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148

```

#### RESULT 14

US-10-294-025-178

; Sequence 178, Application US/10294025

; Publication No. US20030185830A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Stolk, John A.

; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C29

; CURRENT APPLICATION NUMBER: US/10/294, 025

; CURRENT FILING DATE: 2002-11-12

; NUMBER OF SEQ ID NOS: 1038

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 178

; LENGTH: 164

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 118

; OTHER INFORMATION: Xaa = Any Amino Acid

US-10-294-025-178

Query Match 76.1%; Score 577; DB 4; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

```

Qy 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQWVEASLSVRHPEYN 60
; 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQWVEASLSVRHPEYN 60
Db 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPTAGNSCLVSGWGLLNDVAVIAIOSXTV 120
; 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPTAGNSCLVSGWGLLNDVAVIAIOSXTV 120
Qy 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
; 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148
Db 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148

```

#### RESULT 15

US-10-688-838-178

; Sequence 178, Application US/10688838

; Publication No. US20040141989A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; FILE REFERENCE: 210121.427D4

; CURRENT APPLICATION NUMBER: US/10/688, 838

; CURRENT FILING DATE: 2003-10-17

; NUMBER OF SEQ ID NOS: 228

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 178

; LENGTH: 164

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 118

; OTHER INFORMATION: Xaa = Any Amino Acid

US-10-688-838-178

Query Match 76.1%; Score 577; DB 4; Length 164;

Best Local Similarity 77.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

```

Qy 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQWVEASLSVRHPEYN 60
; 1 MENELFCGVLVHPQWVLSAAHCFONSYYTIGLHSLLEADDEPGSQWVEASLSVRHPEYN 60
Db 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPTAGNSCLVSGWGLLNDVAVIAIOSXTV 120
; 61 RPLANDMLIKLDESVESEDPTIRISISIAOCPTAGNSCLVSGWGLLNDVAVIAIOSXTV 120
Qy 116 ----CLPSSRRSSAOSRGLTQSSASQAECPLCC 144
; 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148
Db 121 GGWEC----EKLSQPMQCTTISATSSAR-TSCC 148

```

Search completed: August 29, 2006, 04:05:40

Job time : 178 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2006, 03:38:52 ; Search time 299 Seconds  
(without alignments)  
451.680 Million cell updates/sec

Title: US-10-726-093-10

Sequence: 1 MENELFCSCGLVHPQWVLSA.....SRGLTQSSASQAECPLCCSA 146

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	758	100.0	146	2	Q96JD7_HUMAN	Q96JD7 homo sapien
2	758	100.0	195	2	Q96PT0_HUMAN	Q96PT0 homo sapien
3	577	76.1	131	2	Q96JD8_HUMAN	Q96JD8 homo sapien
4	577	76.1	205	2	Q96JE0_HUMAN	Q96JE0 homo sapien
5	577	76.1	254	1	KLK4_HUMAN	Q9Y5E2 homo sapien
6	577	76.1	254	2	Q4VBI6_HUMAN	Q4VBI6 homo sapien
7	574	75.7	110	2	Q96RU5_HUMAN	Q96RU5 homo sapien
8	574	75.7	159	2	Q96PT1_HUMAN	Q96PT1 homo sapien
9	569	75.1	254	2	Q4VBI7_HUMAN	Q4VBI7 homo sapien
10	566	74.7	205	2	Q96JE2_HUMAN	Q96JE2 homo sapien
11	561	74.0	204	2	Q96JE1_HUMAN	Q96JE1 homo sapien
12	482	63.6	254	2	Q9XSN6_FIG	Q9XSN6 sus scrofa
13	482	59.1	256	2	Q6IEI2_RAT	Q6IEI2 rattus norv
14	431	56.9	255	2	Q9JIS2_MOUSE	Q9JIS2 mus musculu
15	431	56.9	255	2	Q9ZOM1_MOUSE	Q9ZOM1 mus musculu
16	327	43.1	85	2	Q96JD9_HUMAN	Q96JD9 homo sapien
17	285	37.6	204	2	Q96JW8_HUMAN	Q96JW8 homo sapien
18	282	37.2	259	2	Q8IUS5_HUMAN	Q8IUS5 homo sapien
19	282	37.2	293	1	KLK5_HUMAN	Q9YJ37 homo sapien
20	282	37.2	293	1	Q53F68_HUMAN	Q53F68 homo sapien
21	282	37.2	293	2	Q53ZK3_HUMAN	Q53ZK3 mus musculu
22	263	34.7	293	2	Q9DI40_MOUSE	Q9DI40 mus musculu
23	251	33.1	247	2	Q9CPN9_MOUSE	Q9CPN9 mus musculu
24	251	33.1	247	2	Q9D7Y7_MOUSE	Q9D7Y7 mus musculu
25	248	32.7	248	1	TR11_CHICK	Q906Z7 gallus gall
26	248	32.7	248	1	TR12_CHICK	Q906Z8 gallus gall
27	247.5	32.7	242	1	Q7TIR8_YTELE	Q7TIR8 xenopus tro
28	247.5	32.7	260	1	Q3KOI2_XENLA	Q3KOI2 xenopus lae
29	243	32.0	246	1	TRYP_SQUAC	P00764 xenopus aca
30	242.5	32.0	246	1	TR11_CANFA	P06871 canis fami
31	242.5	32.0	253	1	KLK7_HUMAN	P49862 homo sapien

32	242	31.9	243	1	TR11_BOVIN	P00760 bos taurus
33	242	31.9	244	2	Q5EBE2_XENTR	Q5EBE2 xenopus tro
34	241	31.8	247	1	TR13_RAT	P08426 rattus norv
35	241	31.8	248	1	TR13_CHICK	Q90626 gallus gall
36	240.5	31.7	243	2	Q5M959_XENTR	Q5M959 xenopus tro
37	240	31.7	261	2	Q7Z5F4_HUMAN	Q7Z5F4 homo sapien
38	239.5	31.6	178	2	Q5Z0I4_9PERC	Q5Z0I4 xiphister m
39	238.5	31.5	245	2	Q792Y9_MOUSE	Q792Y9 mus musculu
40	238.5	31.5	246	2	Q9Z1R9_MOUSE	Q9Z1R9 mus musculu
41	238.5	31.5	257	1	KLK1_MACFA	Q07276 macaca fasc
42	237.5	31.3	246	2	Q792Y8_MOUSE	Q792Y8 mus musculu
43	237	31.3	231	1	Q6GYJ5_STRUCA	Q6GYJ5 struthio ca
44	237	31.3	246	1	TR12_MOUSE	P07146 mus musculu
45	237	31.3	246	2	Q792Y6_MOUSE	Q792Y6 mus musculu

## ALIGNMENTS

RESULT 1	ID	Q96JD7_HUMAN	PRELIMINARY;	PRT;	146 AA.
AC	Q96JD7;				
DT	01-DEC-2001,	integrated into UniProtKB/TrEMBL.			
DT	01-DEC-2001,	sequence version 1.			
DT	07-FEB-2006,	entry version 23.			
DE	ARM1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	(1)				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Prostate tumor xenograft;				
RX	MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;				
RA	Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saetcioglu F.;				
RT	"Distinctly different gene structure of KLK4/KLK-ii/Protease/ARM1				
RT	compared with other members of the kallikrein family - Pettinuclear				
RT	localization, alternative cDNA forms and regulation by multiple				
RT	hormones."				
RL	DNA Cell Biol. 20:435-445(2001).				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NonDerivs license				
CC	EMBL; AF259970; AAK71705.1; -; mRNA.				
DR	HSSP; 061955; INPM.				
DR	GO; GO:0004252; F-serine-type endopeptidase activity; IEA.				
DR	GO; GO:0005081; P:proteolysis; IEA.				
DR	InterPro; IPR001254; Peptidase_S1_S6.				
DR	InterPro; IPR001314; Peptidase_S1A.				
DR	Pfam; PF00089; Trypsin; 2.				
DR	PRINTS; PR00722; CHYMOTRYPSIN.				
DR	SMART; SM00020; Tryp_Spc; 1.				
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN; 1.				
SQ	SEQUENCE 146 AA; 15512 MW; BBF3A31E0C22C19 CRC64;				
Query Match	100.0%;	Score 758;	DB 2;	Length 146;	
Best Local Similarity	100.0%;	Pred. No. 3.6e-66;			
Matches 146;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MENELFCSCGLVHPQWVLSAHC	PONSYYTIGLHLSLEADQPPGSGMVFASISVVRPEVN	60	
DB	1	MENELFCSCGLVHPQWVLSAHC	PONSYYTIGLHLSLEADQPPGSGMVFASISVVRPEVN	60	
QY	61	RELLANDMLIKLDSVSSEDTIRIS	IASOCPFGNSCLVSGMGLANGELTGVC	120	
DB	61	RELLANDMLIKLDSVSSEDTIRIS	IASOCPFGNSCLVSGMGLANGELTGVC	120	
QY	121	RRSSAQRGLTQSSASQAECPLCCSA	146		
DB	121	RRSSAQRGLTQSSASQAECPLCCSA	146		

Db 121 RRSASQSGVLTOSASQAECCLPCCSA 146

# RESULT 2

096PT0\_HUMAN PRELIMINARY; PRT; 195 AA.  
 ID 096PT0\_HUMAN  
 AC 096PT0\_HUMAN  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-DEC-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 24.  
 DE kallikrein 4 splice variant.  
 GN Name=KLK4;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 CC Homo.  
 CC NCBI\_TaxId=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=9367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;  
 RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;  
 RT "Localization of a new prostate-specific antigen-related serine  
 protease gene, KLK4, is evidence for an expanded human kallikrein gene  
 family cluster on chromosome 19q13.3-13.4.";  
 RT J. Biol. Chem. 274:23210-23214(1999).  
 RL J. Biol. Chem. 274:23210-23214(1999).  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs license

EMBL: AF148532; AAL14782.1; -, Genomic\_DNA.  
 DR HSSP; Q61955; INPM.  
 DR GO; GO:0008236; F:serine-type peptidase activity; ISS.  
 DR GO; GO:0006508; P:proteolysis; ISS.  
 DR InterPro: IPR001254; Peptidase\_S1\_S6.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; Trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 SQ SEQUENCE 195 AA; 20585 MW; EF7E96978B151581 CRC64;

Query Match 100.0%; Score 758; DB 2; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-66;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENELFCSGVLPVHPQWVLSAHCFOVNSYTTGLGLHSLEADPEPGSQWVEASLSVHRPEYN 60  
 Db 50 MENELFCSGVLPVHPQWVLSAHCFOVNSYTTGLGLHSLEADPEPGSQWVEASLSVHRPEYN 109  
 QY 61 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMGLANGELTGVCLPSS 120  
 Db 110 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMGLANGELTGVCLPSS 169  
 QY 121 RRSASQSGVLTOSASQAECCLPCCSA 146  
 Db 170 RRSASQSGVLTOSASQAECCLPCCSA 195

# RESULT 3

096UD8\_HUMAN PRELIMINARY; PRT; 131 AA.  
 ID 096UD8\_HUMAN  
 AC 096UD8\_HUMAN  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-DEC-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 20.  
 DE ARML1 (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 CC Homo.  
 CC NCBI\_TaxId=9606;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Prostate;  
 RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;  
 RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saathcioglu F.;  
 RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARML1  
 RT compared with other members of the kallikrein family - Perinuclear  
 RT localization, alternative CDNA forms and regulation by multiple  
 RT hormones.";  
 RT DNA Cell Biol. 20:435-445(2001).  
 RL  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs license

EMBL: AF259968; AAK71704.1; -, mRNA.  
 DR HSSP; Q61955; INPM.  
 DR Ensemble; ENSG00000167749; Homo sapiens.  
 DR GO; GO:004252; F:serine-type endopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis; IEA.  
 DR InterPro: IPR001254; Peptidase\_S1\_S6.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; Trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 FT NON\_TER 131  
 SQ SEQUENCE 131 AA; 14107 MW; 03434B6D95AF2406 CRC64;

Query Match 76.1%; Score 577; DB 2; Length 131;  
 Best Local Similarity 96.5%; Pred. No. 1.8e-48;  
 Matches 111; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MENELFCSGVLPVHPQWVLSAHCFOVNSYTTGLGLHSLEADPEPGSQWVEASLSVHRPEYN 60  
 Db 1 MENELFCSGVLPVHPQWVLSAHCFOVNSYTTGLGLHSLEADPEPGSQWVEASLSVHRPEYN 60  
 QY 61 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMGLANGELTGV 115  
 Db 61 RPLANDLMLIKLDESSESPTIRISISIASOCPTAGNSCLVSGMGLANGELTGV 115

# RESULT 4

096UE0\_HUMAN PRELIMINARY; PRT; 205 AA.  
 ID 096UE0\_HUMAN  
 AC 096UE0\_HUMAN  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-DEC-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 23.  
 DE ARML1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 CC Homo.  
 CC NCBI\_TaxId=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate tumor xenograft;  
 RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;  
 RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saathcioglu F.;  
 RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARML1  
 RT compared with other members of the kallikrein family - Perinuclear  
 RT localization, alternative CDNA forms and regulation by multiple  
 RT hormones.";  
 RT DNA Cell Biol. 20:435-445(2001).  
 RL  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs license

EMBL: AF259966; AAK71702.1; -, mRNA.  
 DR HSSP; P00760; IEZX.  
 DR Ensemble; ENSG00000167749; Homo sapiens.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.

DR GO; GO:000608; P:proteolysis; IEA.  
 DR InterPro; IPR001254; Peptidase\_S1\_S6.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PRO0722; CHYMOTRYPsin.  
 DR SMART; SM00020; TRYPsin; 1.  
 DR PROSITE; PS02040; TRYPsin; 1.  
 DR PROSITE; PS00134; TRYPsin; 1.  
 DR PROSITE; PS00135; TRYPsin; 1.  
 DR Hydroxylase; Protease; Serine protease.  
 DR SEQUENCE 205 AA; 21950 MW; B83A025C73DBA1F6 CRC64;  
 Query Match 76.1%; Score 577; DB 2; Length 205;  
 Best Local Similarity 96.5%; Pred. No. 3.2e-48;  
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 DB 61 RPLANDLMLIKDESVESDTRISISASQCPAGNSCLVSGMGLANGELTGV 115  
 61 RPLANDLMLIKDESVESDTRISISASQCPAGNSCLVSGMGLANGELTGV 115  
 QY 1 MENELFCGCVLHPQWVLSAHCFOHSYTTGLGLHSLEADQEGSQMVESASVSRHPEN 60  
 1 MENELFCGCVLHPQWVLSAHCFOHSYTTGLGLHSLEADQEGSQMVESASVSRHPEN 60  
 DB 61 RPLANDLMLIKDESVESDTRISISASQCPAGNSCLVSGMGLANGELTGV 115  
 61 RPLANDLMLIKDESVESDTRISISASQCPAGNSCLVSGMGLANGELTGV 115  
 RESULT 5  
 K4\_K4\_HUMAN STANDARD; PRT; 254 AA.  
 AC 09YK2; Q9GZL6; Q9UBU5;  
 DT 01-DEC-2000; Integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1999; sequence version 1.  
 DT 07-FEB-2006; entry version 44.  
 DE Kallikrein-4 precursor (EC 3.4.21.-) (Protease) (Kallikrein-like  
 DE protein 1) (K4-K4) [Ensembl matrix serine proteinase 1].  
 GN Name=K4; Synonyms=EMSP1, PRSS17, PSTS;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=99179024; PubMed=10077646; DOI=10.1073/pnas.96.6.3114;  
 RA Nelson P.S., Gan L., Ferguson C., Moss P., Gellinas R., Hood L.,  
 RA Wang K.;  
 RA "Molecular cloning and characterization of prostate, an androgen-  
 RA regulated serine protease with prostate-restricted expression.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3114-3119(1999).  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=99413477; PubMed=10465467;  
 RA Yousef G.M., Objezu C.V., Luo L.-Y., Black M.H., Diamandis E.P.;  
 RA "Prostate KLK-L1 is a new member of the human kallikrein gene family,  
 RA is expressed in prostate and breast tissues, and is hormonally  
 RA regulated.";  
 RL Cancer Res. 59:4252-4256(1999).  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;  
 RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;  
 RA "Localisation of a new prostate-specific antigen-related serine  
 RA protease gene, KLK4, is evidence for an expanded human kallikrein gene  
 RA family cluster on chromosome 19q13.3-13.4.";  
 RL J. Biol. Chem. 274:23210-23214(1999).  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Moss P., Paepker B., Wang K.;  
 RA "Sequencing and expression analysis of the serine protease gene  
 RA cluster located in chromosome 19q13 region.";  
 RL Gene 257:119-130(2000).  
 RN [5]

RP NUCLEOTIDE SEQUENCE AND CHARACTERIZATION.  
 RX MEDLINE=20322311; PubMed=10863090; DOI=10.1016/S0378-1119(00)00203-1;  
 RX Hu J.C.-C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Stimmer J.P.;  
 RA "Characterization of the mouse and human PRSS17 genes, their  
 RA relationship to other serine proteases, and the expression of PRSS17  
 RA in developing mouse incisors.";  
 RL Gene 251:1-8(2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=prostatic carcinoma; Saetcioglu F.;  
 RA Korkmaz K.S., Korkmaz C.G.,  
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RX PubMed=15057824; DOI=10.1038/nature02399;  
 RX Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,  
 RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,  
 RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,  
 RA Caenepeel S., Carrano A.V., Caole C., Chan Y.M., Christensen M.,  
 RA Cleland C.A., Copeland A., Dalin E., Delal P., Denys M., Deter J.C.,  
 RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,  
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hamon N., Hawkins T.,  
 RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,  
 RA Kobayashi A., Latorov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,  
 RA Maltat S., Martinez D., McCreedy P.M., Medina C., Morgan J.,  
 RA Nelson K., Nolan M., Ovcharenko I., Piatuck S., Pollard M.,  
 RA Popkris A.P., Fredki P., Quan G., Ramirez L., Rash S., Retterer J.,  
 RA Rodrigue A., Rogers S., Salamov A., Salazar A., She X., Smith D.,  
 RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai H., Tsal M., Ustaszewska A.,  
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,  
 RA Furey T.S., DeLong P., Dickson M., Gordon D., Eichler E.E.,  
 RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,  
 RA Rubin E.M., Lucas S.M.;  
 RA "The DNA sequence and biology of human chromosome 19.";  
 RL Nature 428:529-535(2004).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schler N.K.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Scheafer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pang C.C.,  
 RA Raha S.S., Lottiano N.A., Peters G.J., Abramson R.D., Mullen S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
 RA Villalon D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Heaton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Maria M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RA and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE OF 22-254.  
 RP Stimmer J.P., Ryu O.H., Qian Q., Zhang C., Cao X., Sun X., Hu C.-C.;  
 RA "Cloning and characterization of a cDNA encoding human EMSP1.";  
 RL (in) Goldberg M. (eds.);  
 RL Chemistry and biology of mineralized tissues, pp. 1-1, American Academy  
 RL of Orthopaedic Surgeons, Vitell (2000).  
 CC -1- SUBCELLULAR LOCATION: Secreted protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in prostate.  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonCommercial License

```

CC EMBL, AF113140; AAD21580.1; -; mRNA.
DR EMBL, AF113141; AAD21581.1; -; Genomic_DNA.
DR EMBL, AF135023; AAD26424.2; -; Genomic_DNA.
DR EMBL, AF145532; AAD38019.1; -; Genomic_DNA.
DR EMBL, AF243527; AAG33357.1; -; Genomic_DNA.
DR EMBL, AF228497; AAF70620.1; -; Genomic_DNA.
DR EMBL, AF25969; AAF81227.1; -; mRNA.
DR EMBL, AC037199; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL, BC069325; AAH63325.1; -; mRNA.
DR EMBL, BC069403; AAH69403.1; -; mRNA.
DR EMBL, BC069429; AAH69429.1; -; mRNA.
DR EMBL, BC069489; AAH69489.1; -; mRNA.
DR EMBL, AF126401; AAG43246.1; -; mRNA.
DR HSP, P00760; IEZX.
DR MEROPS, S01.251; -.
DR EMBL, ENSG00000167749; Homo sapiens.
DR HGN, HGNC:6365; KLK4.
DR MIM, 603767; gene.
DR GO, GO:0005576; C:extracellular region; TAS.
DR GO, GO:0008236; F:serine-type peptidase activity; NAS.
DR GO, GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro, IPR001254; Peptidase_S1_S6.
DR InterPro, IPR001314; Peptidase_S1A.
DR Pfam, PF00089; Trypsin; 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR SMART, SM00020; TRYP_SPC; 1.
DR PROSITE, PS00240; TRYP_SIN_DOM; 1.
DR PROSITE, PS00134; TRYP_SIN_HIS; 1.
DR PROSITE, PS00135; TRYP_SIN_SER; 1.
DR GlycoProtein, Hydrolyase; Protease; Serine protease; Signal; Zymogen.
KW SIGNAL
FT SIGNAL 1 26 Potential.
FT PROPEP 27 30 Potential.
FT CHAIN 31 254 /FTID=PRO_0000027937.
FT DOMAIN 31 252 /FTID=PRO_0000027938.
FT ACT_SITE 71 71 Charge relay system (by similarity).
FT ACT_SITE 116 116 Charge relay system (by similarity).
FT ACT_SITE 207 207 Charge relay system (by similarity).
FT CARBOHYD 169 169 N-linked (GlcNAc...) (potential).
FT DISULFID 37 167 By similarity.
FT DISULFID 56 72 By similarity.
FT DISULFID 141 241 By similarity.
FT DISULFID 148 213 By similarity.
FT DISULFID 178 192 By similarity.
FT DISULFID 203 228 By similarity.
FT CONFLICT 197 197 O -> H (in Ref. 1 and 4).
SQ SEQUENCE 254 AA; 27023 MW; 9C475E22B6E0C88 CRC64;

Query Match 76.1%; Score 577; DB 1; Length 254;
Best Local Similarity 96.5%; Pred. No. 4.1e-48;
Matches 111; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Maruina K., Farmer A.A., Rabin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
-----
CC EMBL, BC096178; AAH96178.1; -; mRNA.
DR EMBL, BC096175; AAH96175.1; -; mRNA.
DR GO, GO:0008233; F:peptidase activity; IEA.
DR GO, GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO, GO:0006508; P:proteolysis; IEA.
DR InterPro, IPR001254; Peptidase_S1_S6.
DR InterPro, IPR001314; Peptidase_S1A.
DR InterPro, IPR00089; Trypsin; 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR SMART, SM00020; TRYP_SPC; 1.
DR PROSITE, PS00240; TRYP_SIN_DOM; 1.
DR PROSITE, PS00134; TRYP_SIN_HIS; UNKNOWN_1.
DR PROSITE, PS00135; TRYP_SIN_SER; 1.
DR Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 254 AA; 27023 MW; 9C475E22B6E0C88 CRC64;

Query Match 76.1%; Score 577; DB 2; Length 254;
Best Local Similarity 96.5%; Pred. No. 4.1e-48;
Matches 111; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

RESULT 6
ID O4VB16_HUMAN PRELIMINARY; PRT; 254 AA.
AC O4VB16;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Kallikrein 4, preproprotein.
GN Name=KLK4;
OS Homo sapiens (Human).

```

```

RESULT 7
ID O96RUS_HUMAN PRELIMINARY; PRT; 110 AA.
AC O96RUS;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Kallikrein 4, preproprotein.
GN Name=KLK4;
OS Homo sapiens (Human).

```

DE ARM1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
RN NCB1\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;  
RA Kortmaz K.S., Kortmaz C.G., Prellow T.G., Saatchioglou F.;  
RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1  
RT localized with other members of the kallikrein family - Penicillin  
RT localization, alternative cDNA forms and regulation by multiple  
RT hormones";  
RL DNA Cell Biol. 20:435-445(2001).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC  
CC EMBL; AF259971; AAK71706.1; -; mRNA.  
DR HSSP; 061955; INPM.  
DR Ensemble: ENSG00000167749; Homo sapiens.  
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis; IEA.  
DR InterPro; IPR001354; Peptidase\_S1\_S6.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
SQ SEQUENCE 110 AA; 11858 MW; B6F9C135EA93B116 CRC64;  
  
Query Match 75.7%; Score 574; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 2.9e-48;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MENELFCGVLVHPQWVLSAHCFOVNSYITGLGHSLEADQPCGQWVEASLSVRHEYN 60  
DB 1 MENELFCGVLVHPQWVLSAHCFOVNSYITGLGHSLEADQPCGQWVEASLSVRHEYN 60  
  
QY 61 RPLANDLMLIKLDESSESPTIRISIASOCPYAGNSCLVSGWGLANG 110  
DB 61 RPLANDLMLIKLDESSESPTIRISIASOCPYAGNSCLVSGWGLANG 110  
  
RESULT 8  
Q96PT1\_HUMAN PRELIMINARY; PRT; 159 AA.  
ID Q96PT1\_HUMAN  
AC Q96PT1;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 24.  
DE Kallikrein 4 splice variant.  
GN Name=KLK4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
RN NCB1\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;  
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;  
RT "Localization of a new prostate-specific antigen-related serine  
RT protease gene, KLK4, is evidence for an expanded human kallikrein gene  
RT family cluster on chromosome 19q13.3-13.4.";  
RL J. Biol. Chem. 274:23210-23214(1999).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC  
CC EMBL; AF148532; AAL14781.1; -; Genomic\_DNA.

DR HSSP; 061955; INPM.  
DR Ensemble: ENSG00000167749; Homo sapiens.  
DR GO; GO:0008236; F:serine-type peptidase activity; ISS.  
DR GO; GO:0006508; P:proteolysis; ISS.  
DR InterPro; IPR001254; Peptidase\_S1\_S6.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
SQ SEQUENCE 159 AA; 16931 MW; 3CC6BF491B6CA5A CRC64;  
  
Query Match 75.7%; Score 574; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 4.6e-48;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MENELFCGVLVHPQWVLSAHCFOVNSYITGLGHSLEADQPCGQWVEASLSVRHEYN 60  
DB 50 MENELFCGVLVHPQWVLSAHCFOVNSYITGLGHSLEADQPCGQWVEASLSVRHEYN 109  
  
QY 61 RPLANDLMLIKLDESSESPTIRISIASOCPYAGNSCLVSGWGLANG 110  
DB 110 RPLANDLMLIKLDESSESPTIRISIASOCPYAGNSCLVSGWGLANG 159  
  
RESULT 9  
Q4VB17\_HUMAN PRELIMINARY; PRT; 254 AA.  
ID Q4VB17\_HUMAN  
AC Q4VB17;  
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Kallikrein 4, preproprotein.  
GN Name=KLK4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
RN NCB1\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RX TISSUE=PCR rescued clones; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klaukner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshyuk S., Carninci P., Mullany S.J.,  
RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,  
RA Rodriguez A.C., Greenwood J., Schmutz J., Skalska U., Smalhus D.E.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch J., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC  
CC NIH MCC Project;  
CC Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

```
DR EMBL; BC096177; AAH96177.1; -, mRNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE 254 AA; 27053 MW; 1C670B2B3B5E5A5E CRC64;

Query Match 75.1%; Score 569; DB 2; Length 254;
Best Local Similarity 95.7%; Pred. No. 2, 5e-47;
Matches 110; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 50 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 109
OY 61 RPLANDLMLIKLDESSESDDTIRISISASQCPAGNSCLVSGWGLLANGELTGV 115
DB .110 RPLANDLMLIKLDESSESDDTIRISISASQCPAGNSCLVSGWGLLANGRMPTV 164

RESULT 10
O96JEL_HUMAN PRELIMINARY; PRT; 205 AA.
AC O96JEL;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE ARM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Preclow T.G., Saaticoglu F.;
RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones."
RL DNA Cell Biol. 20:435-445(2001).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial license
CC
CC EMBL; AF25964; AAK71700.1; -, mRNA.
DR HSSP; P00760; IEZX.
DR Ensemble; ENSG00000167749; Homo sapiens.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE 205 AA; 22052 MW; 159B61A20D94BD57 CRC64;

Query Match 74.7%; Score 566; DB 2; Length 205;
```

```
Best Local Similarity 94.8%; Pred. No. 3, 8e-47;
Matches 109; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
OY 61 RPLANDLMLIKLDESSESDDTIRISISASQCPAGNSCLVSGWGLLANGELTGV 115
DB 61 RPLANDLMLIKLDESSESDDTIRISISASQCPAGNSCLVSGWGLLANGRMPTV 115

RESULT 11
O96JEL_HUMAN PRELIMINARY; PRT; 204 AA.
AC O96JEL;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE ARM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Preclow T.G., Saaticoglu F.;
RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones."
RL DNA Cell Biol. 20:435-445(2001).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial license
CC
CC EMBL; AF25965; AAK71701.1; -, mRNA.
DR HSSP; P00760; IEZX.
DR Ensemble; ENSG00000167749; Homo sapiens.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE 204 AA; 21811 MW; 45742165D23A53F3 CRC64;

Query Match 74.0%; Score 561; DB 2; Length 204;
Best Local Similarity 98.2%; Pred. No. 1, 2e-46;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
DB 1 MENELFCGVLVHPQWLSAAHCFONSYYTIGLHSLADQEPGQWVEASLSVRHPEYN 60
OY 61 RPLANDLMLIKLDESSESDDTIRISISASQCPAGNSCLVSGWGLLANG 110
DB 61 RPLANDLMLIKLDESSESDDTIRISISASQCPAGNSCLVSGWGLLANG 110

RESULT 12
O9XSN6_PIG PRELIMINARY; PRT; 254 AA.
AC O9XSN6;
```







DR Ensembl; ENSMUSG0000006948; Mus musculus.  
 DR MGI; MGI:1861379; K1k4.  
 DR GO; GO:0005615; Cytoplasmic space; RCA.  
 DR GO; GO:0004263; F-tyrosinase activity; RCA.  
 DR GO; GO:0004295; F-tyrosinase activity; RCA.  
 DR GO; GO:000508; P-proteinase; RCA.  
 DR InterPro; IPR001254; Peptidase\_S1\_S6.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; Tyrosin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Hydrolase; Protease; Serine protease; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 32 255  
 SQ SEQUENCE 255 AA; 27536 MW; CBF5FBAF7DAD679C CRC64;  
 Query Match 56.9%; Score 431; DB 2; Length 255;  
 Best Local Similarity 63.6%; Pred. No. 9e-34;  
 Matches 82; Conservative 18; Mismatches 27; Indels 2; Gaps 1;  
 QY 2 ENELFCGSLVHPQWVLSAHCFCNSYTGILGHSLEADQEPGSGWVSEASLVREHYNR 61  
 DB 52 EDGFCGSLVHPQWVLSAHCFCNSYTGILGHSLEADQEPGSGWVSEASLVREHYNR 111  
 QY 62 PLIANDMLIKLDESSESSTIRISIASQCTPAGNSCLVSGWGLANGELNGV--CLPS 119  
 DB 112 PSFANDMLIKLDESSESSTIRISIVATQCPTPDCTLVSGWGLKNGKLPGLQCNVL 171  
 QY 120 SRRSSAQR 128  
 DB 172 SVASEETCR 180  
 RESULT 15  
 Q9ZOM1\_MOUSE PRELIMINARY; PRT; 255 AA.  
 AC Q9ZOM1  
 DT 01-MAY-1999; Integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-1999; sequence version 1.  
 DT 07-FEB-2006; entry version 36.  
 DE Enamel matrix serine proteinase 1 precursor (Kallikrein 4) (Protease,  
 DE Enamel matrix, prostatic).  
 GN Name=K1k4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Swiss-Webster;  
 RX MEDLINE=202323211; PubMed=10863090; DOI=10.1016/S0378-1119(00)00203-1;  
 RA Hu J.C.-C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;  
 RT "Characterization of the mouse and human PRSS17 genes, their  
 RT relationship to other serine proteases, and the expression of PRSS17  
 RT in developing mouse incisors.";  
 RL Gene 251:1-8(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Swiss-Webster;  
 RX MEDLINE=20152522; PubMed=10690663;  
 RA Hu J.C.-C., Ryu O.H., Chen J.J., Uchida T., Wakida K., Murakami C.,  
 RA Jiang H., Qian Q., Zhang C., Ottmers V., Bartlett J.D., Simmer J.P.;  
 RT "Localization of Emspi expression during tooth formation and cloning  
 RT of mouse cDNA.";  
 RL J. Dent. Res. 79:70-76(2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Swiss-Webster;  
 RA Simmer J.;

RT "Enamel Matrix Serine Proteinase 1 (EMSP1)";  
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carlini P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RG NIH MGC Project;  
 RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonCommercial license  
 CC -----  
 DR EMBL; AF019979; AAC98894.1; -; mRNA.  
 DR EMBL; BC100717; AA100718.1; -; mRNA.  
 DR EMBL; BC100718; AA100719.1; -; mRNA.  
 DR EMBL; BC100716; AA100717.1; -; mRNA.  
 DR EMBL; BC100719; AA100720.1; -; mRNA.  
 DR HSP; P00760; 1EXZ.  
 DR MEROPS; S01.251; -.  
 DR Ensembl; ENSMUSG0000006948; Mus musculus.  
 DR MGI; MGI:1861379; K1k4.  
 DR GO; GO:0005615; Cytoplasmic space; RCA.  
 DR GO; GO:0004263; F-tyrosinase activity; RCA.  
 DR GO; GO:0004295; F-tyrosinase activity; RCA.  
 DR GO; GO:000508; P-proteinase; RCA.  
 DR InterPro; IPR001254; Peptidase\_S1\_S6.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; Tyrosin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Hydrolase; Protease; Serine protease; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 32 255  
 SQ SEQUENCE 255 AA; 27488 MW; 6FD2E7DEA060A2A CRC64;  
 Query Match 56.9%; Score 431; DB 2; Length 255;  
 Best Local Similarity 63.6%; Pred. No. 9e-34;  
 Matches 82; Conservative 18; Mismatches 27; Indels 2; Gaps 1;  
 QY 2 ENELFCGSLVHPQWVLSAHCFCNSYTGILGHSLEADQEPGSGWVSEASLVREHYNR 61  
 DB 52 EDGFCGSLVHPQWVLSAHCFCNSYTGILGHSLEADQEPGSGWVSEASLVREHYNR 111  
 QY 62 PLIANDMLIKLDESSESSTIRISIASQCTPAGNSCLVSGWGLANGELNGV--CLPS 119  
 DB 112 PSFANDMLIKLDESSESSTIRISIVATQCPTPDCTLVSGWGLKNGKLPGLQCNVL 171

Qy	120	SRSSAOSR	128
Db	172	SVASEETCR	180

Search completed: August 29, 2006, 03:47:02  
Job time : 302 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 28, 2006, 18:09:34 ; Search time 3295 Seconds  
(without alignments)

4250.223 Million cell updates/sec

Title: US-10-726-093-10

Perfect score: 758  
Sequence: 1 MENELFCGVLVHPQWLISA.....SRGLTQSSAQAECLPCCSA 146

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying Chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame\_plus.p2n.model -DEV=xlp  
-O=/abs/ABSSWEB-SPool/US10726093/runat\_28082006\_121135\_25575/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -DOORCL=0 -DOOREXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05p  
-USER=US10726093 @GCN 1 1 8328 @runat\_28082006\_121135\_25575 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEC\_SCORES=0 -WAIT\_DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:1\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vl:\*  
11: gb\_ov:\*  
12: gb\_hcg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758	100.0	702	2	AX052869 Sequence
2	758	100.0	702	5	AF259970 Homo sapi
3	758	100.0	1265	2	BD070317 Compounds

4	758	100.0	1265	2	BD242081
5	758	100.0	1265	2	AR237264
6	758	100.0	1265	2	AR278288
7	758	100.0	1265	2	AR366984
8	758	100.0	1265	2	AR370880
9	758	100.0	1265	2	AR392385
10	758	100.0	1265	2	AR400020
11	758	100.0	1265	2	AR439491
12	758	100.0	1265	2	AR563667
13	758	100.0	1265	2	AR588653
14	758	100.0	1265	2	AR605473
15	758	100.0	1265	2	AR653087
16	758	100.0	1265	2	AR656812
17	758	100.0	1265	2	AR716719
18	758	100.0	1265	2	AX106392
19	758	100.0	1265	2	AX140683
20	758	100.0	1265	2	AX200543
21	758	100.0	1265	2	AX267199
22	758	100.0	1265	2	AX052876
23	730	96.3	701	2	AX969474
24	695	91.7	484	2	BD108193
25	695	91.7	484	2	BD108193
26	695	91.7	484	2	BD108193
27	660	87.1	4385	5	AF148532
28	660	87.1	4740	5	AF135023
29	660	87.1	5900	5	AF113141
30	660	87.1	7115	5	AF228497
31	660	87.1	40466	12	AC135047
32	660	87.1	217346	12	AC027602
33	660	87.1	230000	5	AF243527
34	652	86.0	107487	5	AC011483
35	640	84.4	1459	2	BD070318
36	640	84.4	1459	2	BD242082
37	640	84.4	1459	2	AR237265
38	640	84.4	1459	2	AR278289
39	640	84.4	1459	2	AR366985
40	640	84.4	1459	2	AR370881
41	640	84.4	1459	2	AR392386
42	640	84.4	1459	2	AR400021
43	640	84.4	1459	2	AR405288
44	640	84.4	1459	2	AR439492
45	640	84.4	1459	2	AR563668

#### ALIGNMENTS

RESULT 1	AX052869	702 bp	DNA	linear	PAT 12-JAN-2001
AX052869	Sequence 3 from Patent WO0071711.				
DEFINITION	AX052869				
ACCESSION	AX052869.1	GI:12226978			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homnidae; Homo.				

REFERENCE	1
AUTHORS	Saatioglu, F.
TITLE	Differentially expressed genes in prostate cancer
JOURNAL	Patent: WO 0071711-A 3 30-NOV-2000;
	Saatioglu, F.
FEATURES	Location/Qualifiers
source	1..702
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"

#### ORIGIN

Alignment Scores:	5.3e-65	Length:	702
Pred. No.:	758.00	Matches:	146
Score:			

Percent Similarity: 100.0%  
Best. Local Similarity: 100.0%  
Query Match: 100.0%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-10-726-093-10 (1-146) x AX052869 (1-702)

QY 1 MetGluasnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 1 ATGGAAGAAAGCAATGTTGCTGCTCGGGCTCTGCTGATCCGACGATGGGTCTCTCAGCC 60  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 61 GCACACGTTTCCAGAACTCCTACACCATCGGCTGGCTGCACAGCTTTGAGCCGAC 120  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 121 CAAAGCCAGGAGCCAGATGTGAGGCGACCTCTCCGACGACCCAGAGTACAC 180  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGluSer 80  
DB 181 AGACCTTGTCTCGCTAAGACCTCATGCTCATCAAGTTGAGCGAATCGGTCTCGAGTCT 240  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 241 GACACCATCCGAGCATCAGCATGCTTCCGAGTCCCTACCGCGGGGAACTTTGCTC 300  
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 301 GTTTCGTGGCTGGGTCTGCTGCGAAGCGTGAAGCTCAGGGGTGTGTCTGCTCTTCA 360  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140  
DB 361 AGGAGTCTCTGCTGCGACGTTGAGCTCAGGGGTGTGTCTGCTCTTCA 420  
QY 141 LeuProCysCysSerAla 146  
DB 421 CTACCGTGTCTGCAGTGCG 438

RESULT 2  
LOCUS AF259970 702 bp mRNA linear PRI 02-AUG-2001  
DEFINITION Homo sapiens ARM1 mRNA, alternatively spliced, complete cds.  
ACCESSION AF259970  
VERSION AF259970.1 GI:14646878  
KEYWORDS

## ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 702)  
Korkmaz, K.S., Korkmaz, C.G., Prejlow, T.G. and Saatchioglou, F.  
Distinctly Different Gene Structure of KLK4/KLK-14/Prostate/ARML  
Compared with Other Members of the Kallikrein Family: Intracellular  
Localization, Alternative CDNA Forms, and Regulation by Multiple  
Hormones  
DNA Cell Biol. 20 (7), 435-445 (2001)

## REFERENCE

AUTHORS

TITLE

JOURNAL PUBMED 11506707  
2 (bases 1 to 702)  
Korkmaz, K.S., Korkmaz, C.G. and Saatchioglou, F.  
Direct Submission  
Submitted (24-APR-2000) Biotechnology Center of Oslo, University of  
Oslo, Gaustadalleen 21, Oslo 0349, Norway  
Location/Qualifiers

## FEATURES

SOURCE

1. 702  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="prostate tumor xenograft (CWR22)"  
1. 441  
/experiment="experimental evidence, no additional details  
recorded"

/note="ARM1V, alternatively spliced"  
/codon\_start=1  
/product="ARM1"  
/protein\_id="AAK71705.1"  
/db\_xref="GI:14646879"  
/translation="MENELFCGSLVHPQWVLSAHCPSNYTIGLHSLLEADQERG  
SQWENSLVSRHPVIRPLANDMLIKDESYSBSDTIRISIASQCFPAGNSCLVS  
GMGLANGELGVCLPSSRRSSAQSRLGTQSSAQAECLPCCSA"

## ORIGIN

## Alignment Scores:

Pred. No.: 5,3e-65 Length: 702  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatch: 0  
Query Match: 100.0% Indels: 0  
DB: 5 Gaps: 0

US-10-726-093-10 (1-146) x AF259970 (1-702)

QY 1 MetGluasnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 1 ATGGAAGAAAGCAATGTTGCTGCTCGGGCTCTGCTGATCCGACGATGGGTCTCTCAGCC 60  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 61 GCACACGTTTCCAGAACTCCTACACCATCGGCTGGCTGCACAGCTTTGAGCCGAC 120  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 121 CAAAGCCAGGAGCCAGATGTGAGGCGACGCTCTCCGACGACCCAGAGTACAC 180  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGluSer 80  
DB 181 AGACCTTGTCTCGCTAAGACCTCATGCTCATCAAGTTGAGCGAATCGGTCTCGAGTCT 240  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 241 GACACCATCCGAGCATCAGCATGCTTCCGAGTCCCTACCGCGGGGAACTTTGCTC 300  
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 301 GTTTCGTGGCTGGGTCTGCTGCGAAGCGTGAAGCTCAGGGGTGTGTCTGCTCTTCA 360  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140  
DB 361 AGGAGTCTCTGCTGCGACGTTGAGCTCAGGGGTGTGTCTGCTCTTCA 420  
QY 141 LeuProCysCysSerAla 146  
DB 421 CTACCGTGTCTGCAGTGCG 438

RESULT 3  
LOCUS BD070317 1265 bp DNA linear PAT 27-AUG-2002  
DEFINITION Compounds for immunodiagnosis of prostate cancer and methods for  
their use.

## ACCESSION

BD070317

VERSION

BD070317.1 GI:22615920

KEYWORDS

JP 2001513886-A/168.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 1265)  
Xu, J. and Dillon, D.C.  
Compounds for immunodiagnosis of prostate cancer and methods for  
their use  
Patent: JP 2001513886-A 168 04-SEP-2001;  
CORIXA CORP  
OS Homo sapiens (human)  
PN JP 2001513886-A/168

## REFERENCE

AUTHORS

TITLE

JOURNAL  
OS  
COMMENT

PD 04-SEP-2001  
 PF 25-FEB-1998 JP 1998537008  
 PR 25-FEB-1997 US 08/806596.01-AUG-1997 US 08/904809 PR  
 09-FEB-1998 US 09/020747  
 PI JIANGCHUN XU DAVIN C DILLON  
 PC GOIN33/574,GOIN33/577,C07K16/30,A61K39/395,A61K47/48,C12Q1/68,  
 PC GOIN33/543  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 CC Compounds for immunodiagnosis of prostate cancer and methods  
 for their use  
 FH Key Location/Qualifiers  
 FT source 1..1265  
 Location/Qualifiers  
 1..1265  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 9,47e-65 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x BD070317 (1-1265)

QY 1 MetGLUaenGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAAAACGAATTGTTCTGCTCGGCGCTGTCATCCGACGAGGCTGTGAGCC 99  
 QY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40  
 DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGCTGCGCTGACAGTCTTGAGGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGlnAlaSerLeuSerValArgHisProGlnTyra 60  
 DB 160 CAAGACCCAGGAGCCAGATGTGAGGCCACTCTCCCTAAGGACCCAGAGTCAAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnSer 80  
 DB 220 AGACCTTGTGCTTAACGACCTTCATGCTCATCAAGTGGACGAATCCGTGTCGAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCATCCGAGCATCAGCAATGCTTCCAGATGCCCTACCGGGGGAACCTTGCTC 339  
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTTCGGCTGGGCTCTGCTGCGACAGCTGAGCTCAGGGTGTGTCTGCCCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140  
 DB 400 AGAGAGTCTCTCCCTCCAGCTCGCGGGGCTGACCCAGAGCTCTGCTCCAGAGATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTGTGACGATGCG 477

## RESULT 4

BD242081 1265 bp DNA linear PAT 17-JUL-2003  
 LOCUS BD242081 1265 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Compounds for immunotherapy and diagnosis of prostate cancer and  
 methods for their use.

ACCESSION BD242081  
 VERSION BD242081.1 GI:33051851  
 KEYWORDS UP 2002520054-A/168.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 1265)  
 DILLON,D.C., HARLOCKER,S.L., YUQIU,J., XU,J. and MITCHAM,J.L.  
 Compounds for immunotherapy and diagnosis of prostate cancer and  
 methods for their use  
 Patent: JP 2002520054-A 168 09-JUL-2002;  
 JOURNAL CORIXA CORP  
 OS Homo sapiens (human)  
 PN JP 2002520054-A/168  
 PD 09-JUL-2002  
 PF 14-JUL-1999 JP 2000560247  
 PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR  
 23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR  
 15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR  
 09-APR-1999 US 09/288946  
 PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI  
 JIANGCHUN XU,  
 PI JENNIFER LYNN MITCHAM

## COMMENT

PC C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,  
 PC C12N5/10,  
 PC C12P21/08,C12Q1/68,GOIN33/574,GOIN33/68//A61P35/00,C12N15/00,  
 PC A61K37/02,  
 PC C12N5/00  
 CC n = A,T,C or G  
 FH Key Location/Qualifiers  
 FT misc\_feature (1)..(1265).  
 Location/Qualifiers  
 1..1265  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

## FEATURES

source

## ORIGIN

Alignment Scores:  
 Pred. No.: 9,47e-65 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 2 Gaps: 0

US-10-726-093-10 (1-146) x BD242081 (1-1265)

QY 1 MetGLUaenGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAAAACGAATTGTTCTGCTCGGCGCTGTCATCCGACGAGGCTGTGAGCC 99  
 QY 21 AlaHisCysPheGlnAsnSerTyrrThrIleGlyLeuGlyLeuHisSerLeuGlnAlaAsp 40  
 DB 100 GCACACTGTTTCCAGAACTCTTACACCATCGGCTGCGCTGACAGTCTTGAGGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGlnAlaSerLeuSerValArgHisProGlnTyra 60  
 DB 160 CAAGACCCAGGAGCCAGATGTGAGGCCACTCTCCGTACGAGCACCAGAGTCAAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnSer 80  
 DB 220 AGACCTTGTGCTTAACGACCTTCATGCTCATCAAGTGGACGAATCCGTGTCGAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCATCCGAGCATCAGCAATGCTTCCAGATGCCCTACCGGGGGAACCTTGCTC 339  
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTTCGGCTGGGCTCTGCTGCGACAGCTGAGCTCAGGGTGTGTCTGCCCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140  
 DB 400 AGAGAGTCTCTCCCTCCAGCTCGCGGGGCTGACCCAGAGCTCTGCTCCAGAGATGC 459

OY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTGTCTGCGAGTGGC 477

RESULT 5  
LOCUS AR237264 1265 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 173 from patent US 6465611.  
ACCESSION AR237264  
VERSION AR237264.1 GI:27281922  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1265)  
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.  
TITLE Compounds for immunotherapy of prostate cancer and methods for their use  
JOURNAL Patent: US 6465611-A 173 15-OCT-2002;  
Corixa Corporation; Seattle, WA

FEATURES  
source 1..1265  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 9,47e-65 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0

US-10-726-093-10 (1-146) x AR237264 (1-1265)

OY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAGCGAATGTTCTGCTGGCGGCGTCTGTCGATCCGCACTGGAGTCTGTCAAGC 99

OY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTTCCAGAACTCTCAACCACTGGGCTGGGCTGCACAGCTTGAGGCCGAC 159

OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60  
DB 160 CAAGAGCCAGGAGGAGCGATGGTGGAGGCGAGCTCTCCGTACGGCACCAGATACAC 219

OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGTCTGCTCAACGACCTCACTGCTCATCAAGTTGAGAGATCCGTCTCCAGTCT 279

OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCACTCCGAGCATCGACTTCTTCCAGTCTCCCTCAACCGGGAACTCTTGCTTC 339

OY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTCTGTGCTGGCGTCTGCTGGCGAAGCGTGAAGTCAAGGAGTGTGTCTGCTCTTCA 399

OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGGAGGTCTCTGCGCAGTCCGCGGGGCTGAGCCAGACCTGTGCTCCAGGAGCAATGC 459

OY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTGTCTGCGAGTGGC 477

RESULT 6  
LOCUS AR278288 1265 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 173 from patent US 6512094.  
ACCESSION AR278288

VERSION AR278288.1 GI:29712534  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1265)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kallou,M.D., Fanger,G.R., Rector,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6512094-A 173 28-JAN-2003;  
Corixa Corporation; Seattle, WA

FEATURES  
source 1..1265  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 9,47e-65 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0

US-10-726-093-10 (1-146) x AR278288 (1-1265)

OY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 100 GCACACTGTTTCCAGAACTCTCAACCACTGGGCTGGGCTGCACAGTCTTGAGGCCGAC 159

OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60  
DB 160 CAAGAGCCAGGAGGAGCGAATGGTGGAGGCGAGCTCTCCGTACGGCACCAGATACAC 219

OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGTCTGCTCAACGACCTCACTGCTCATCAAGTTGAGAGATCCGTCTCCAGTCT 279

OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCACTCCGAGCATCGACTTCTTCCAGTCTCCCTCAACCGGGGAACTCTTGCTTC 339

OY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTCTGTGCTGGCGTCTGCTGGCGAAGCGTGAAGTCAAGGAGTGTGTCTGCTCTTCA 399

OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGGAGGTCTCTGCGCAGTCCGCGGGGCTGAGCCAGACCTGTGCTCCAGGAGCAATGC 459

OY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTGTCTGCGAGTGGC 477

RESULT 7  
LOCUS AR366984 1265 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 173 from patent US 6329505.  
ACCESSION AR366984  
VERSION AR366984.1 GI:34599959  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1265)

## AUTHORS

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yagin, J.,  
Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. and  
Day, C.H.

## TITLE

Compositions and methods for therapy and diagnosis of prostate  
cancer

## JOURNAL

Patent: US 6329505-A 173 11-DEC-2001;  
Corixa Corporation, Seattle, WA

## FEATURES

Location/Qualifiers  
1..1265  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
9.47e-65	1265	146	0	0	0	0
Percent Similarity:	100.0%					
Best Local Similarity:	100.0%					
Query Match:	100.0%					

US-10-726-093-10 (1-146) x AR366984 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAACGAATTGTTCTCTGCTGGCGGCTCTGTCATCCGACATGGAGTGTCTGACGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTTACACCTCCTGACATCCGAGCTGGGCTGCTGACAGCTTGAAGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 160 CAAAGCCAGGAGGAGCAGATGTGTGAGGCGACCTCTCCGTAAGGACACCAAGTAAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGTCTGCTGCTACACCTCCTGCTCATCAAGTTGAGCAATCCCTGTCCAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGAGGAGCATGCAATGCTTTCGACGTGCTCACCCTTCCGCGGGAACCTTGGCCTC 339  
QY 101 ValSerGlyTyrPglYLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTTCGTGCTGGGCTCTGCTGCGAACGCTGAGCTCAGCGGTGTGTCTGCTGCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGGAGGTCTCTGCTGCTGCGGAGGCTGACCCAGACCTTGTGCTCCAGGCGAGATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCTGAGTGC 477

## RESULT 8

AR370880 AR370880 1265 bp DNA linear PAT 12-SEP-2003

## LOCUS

Sequence 173 from patent US 6395278.

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

1 (bases 1 to 1265)  
Unclassified.

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L. and Yagin, J.

Prostate specific fusion protein compositions

Patent: US 6395278-A 173 28-MAY-2002;

Corixa Corporation, Seattle, WA

Location/Qualifiers

1..1265

/organism="unknown"

## ORIGIN

/mol\_type="genomic DNA"

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
9.47e-65	1265	146	0	0	0	0
Score:	758.00					
Percent Similarity:	100.0%					
Best Local Similarity:	100.0%					
Query Match:	100.0%					

US-10-726-093-10 (1-146) x AR370880 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAACGAATTGTTCTCTGCTGGCGGCTCTGTCATCCGACATGGAGTGTCTGACGCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTTACACCTCCTGACATCCGAGCTGGGCTGCTGACAGCTTGAAGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 160 CAAAGCCAGGAGGAGCAGATGTGTGAGGCGACCTCTCCGTAAGGACACCAAGTAAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGTCTGCTGCTACACCTCCTGCTCATCAAGTTGAGCAATCCCTGTCCAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGAGGAGCATGCAATGCTTTCGACGTGCTCACCCTTCCGCGGGAACCTTGGCCTC 339  
QY 101 ValSerGlyTyrPglYLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTTCGTGCTGGGCTCTGCTGCGAACGCTGAGCTCAGCGGTGTGTCTGCTGCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGGAGGTCTCTGCTGCTGCGGAGGCTGACCCAGACCTTGTGCTCCAGGCGAGATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCTGAGTGC 477

## RESULT 9

AR392385 AR392385 1265 bp DNA linear PAT 18-DEC-2003

## LOCUS

Sequence 173 from patent US 6613872.

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

1 (bases 1 to 1265)  
Unclassified.

Xu, J. and Dillon, D.C.

Compounds for immunotherapy of prostate cancer and methods for  
their use

Patent: US 6613872-A 173 02-SEP-2003;

Corixa Corporation, Seattle, WA

Location/Qualifiers

1..1265

/organism="unknown"

/mol\_type="genomic DNA"

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
9.47e-65	1265	146	0	0	0
Score:	758.00				
Percent Similarity:	100.0%				
Best Local Similarity:	100.0%				
Query Match:	100.0%				

[illegible]

Db	Accession	Length	Score	Percent Similarity	Best Local Similarity	Query Match	DBs
Db	40	ATGGAAGAACAAATGTTCTCTCTCGGCGCTCTGGTGCATCCGACGTGGGTCTGTACAGCC	9.47e-65	758.00	100.0%	100.0%	1
Qy	21	AlaHisGysPheGlnAsnSerTrpThrIleGlyValenGlyLeuHisSerLeuGluAlaAsp	1265	146	0	0	20
Db	100	GCACACGTGTTCCAGAACTCTTACACCATCGGGGTGGGCTGCACACTCTTGAAGCCGAC	9.47e-65	758.00	100.0%	100.0%	1
Qy	41	GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaArgHisProGluTrpAsn	1265	146	0	0	20
Db	160	CAAGAGCCAGGAGGCCAGATGTGTGAGGCGCAGCCTCTCCGTACGGCACCCAGAGTACAC	9.47e-65	758.00	100.0%	100.0%	1
Qy	61	ArgProteinLeuAlaAsnAspLeuMetLeuIleGlyLeuAsnAspGluSerValSerGluSer	1265	146	0	0	20
Db	220	AGACCTTGCTGCTGTAACGACCTCATAGCTCATACAGTGGACGATCCGATCCGATCT	9.47e-65	758.00	100.0%	100.0%	1
Qy	81	AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu	1265	146	0	0	20
Db	280	GACACCATCCGGAGCATTACCATTTGCTTGCAGTGGCCCTACCGGGGAACTTGTGCTC	9.47e-65	758.00	100.0%	100.0%	1
Qy	101	ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer	1265	146	0	0	20
Db	340	GTTCCTGCTGCGGGGTCTGCTGGGAGCGGTGACCTACCGGGTGTGTCTGCTCTTCA	9.47e-65	758.00	100.0%	100.0%	1
Qy	121	ArgArgSerSerArgGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys	1265	146	0	0	20
Db	400	AGGAGGTCCTCTGCTGCCAGTCCGGGGGCTACCCAGAGCTCTGCTGCCAGGACGATGC	9.47e-65	758.00	100.0%	100.0%	1
Qy	141	LeuProCysCysSerAla 146	1265	146	0	0	20
Db	460	CTACCGTGTCTGCTGAGTGGC 477	9.47e-65	758.00	100.0%	100.0%	1
RESULT 11	AR405287	1265 bp	DNA	linear	PAT 18-DEC-2003		
LOCUS	AR405287	1265 bp	DNA	linear	PAT 18-DEC-2003		
DEFINITION	Sequence 173 from patent US 6630305.						
ACCESSION	AR405287						
VERSION	AR405287.1						
KEYWORDS	GI:40154124						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	Unclassified.						
AUTHORS	1 (Dases 1 to 1265)						
	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,						
	Kalos,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,						
	Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,						
	Hepler,W.T. and Henderson,R.A.						
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer						
JOURNAL	Patent: US 6630305-A 173 07-OCT-2003;						
	Cotix Corporation, Seattle, WA;						
	MOX;						
FEATURES	Location/Qualifiers						
SOURCE	1..1265						
	/organism="unknown"						
	/mol_type="genomic DNA"						
ORIGIN							
Alignment Scores:	9.47e-65	Length:	1265				
Score:	758.00	Matches:	146				
Percent Similarity:	100.0%	Conservative:	0				
Best Local Similarity:	100.0%	Mismatches:	0				
Query Match:	100.0%	Indels:	0				
DBs:	2	Gaps:	0				
US-10-726-093-10 (1-146) x AR405287 (1-1265)							
Qy	1	MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla	1265	146	0	0	20
Db	40	ATGGAAGAACAAATGTTCTCTCTCGGCGCTCTGGTGCATCCGACGTGGGTCTGTACAGCC	9.47e-65	758.00	100.0%	100.0%	1
Qy	21	AlaHisGysPheGlnAsnSerTrpThrIleGlyValenGlyLeuHisSerLeuGluAlaAsp	1265	146	0	0	20
Db	100	GCACACGTGTTCCAGAACTCTTACACCATCGGGGTGGGCTGCACACTCTTGAAGCCGAC	9.47e-65	758.00	100.0%	100.0%	1
Qy	41	GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaArgHisProGluTrpAsn	1265	146	0	0	20



QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 160 CAAGAGCGCAGGAGACCGAGATGTTGAGGCCCTCCGTAAGCGGACCCAGAGTAAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGCTGCGTAAAGACATCATGCTCATCAAGTTGGACGAATCCGTGTCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGACCATCAGCATGCTTCGACATGCCCTACCGCGGGGAATCTTGCTC 339  
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTCTGGCTGGGCTGCTGCTGCGACGCGTGAAGCTCAGCGGTGTGTGCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGGAGGTCTCTGCGCCAGTCCGCGGGGCTGACCCAGACATCTGCGTCCAGAGCAATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCAAGTGC 477  
RESULT 12  
AR439491 1265 bp DNA linear PAT 20-FEB-2004  
LOCUS AR439491 Sequence 173 from patent US 6664377.  
DEFINITION AR439491  
ACCESSION AR439491  
VERSION AR439491.1 GI:42665400  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1265)  
AUTHORS Xu, J.  
TITLE Compounds for immunotherapy of prostate cancer and methods for their use  
JOURNAL Patent: US 6664377-A 173 16-DEC-2003;  
Corixa Corporation; Seattle, WA;  
FEATURES  
source Location/Qualifiers  
1..1265  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores: 9,47e-65 Length: 1265  
Pred. No.: 758.00 Matches: 146  
Score: 100.0% Conservative: 0  
Percent Similarity: 100.0% Mismatches: 0  
Best Local Similarity: 100.0% Indels: 0  
Query Match: 2 Gaps: 0  
DB: 2  
US-10-726-093-10 (1-146) x AR439491 (1-1265)  
QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTyrValLeuSerAla 20  
DB 40 ATGGAAGAAACGAATTTGTTCTGCTCGGGCGCTCTGGTGATCCGACATGGGTGCTGACCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTACACATCGGGCTGGGCTGCACAGTCTTGAAGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 160 CAAGAGCGCAGGAGACCGAGATGTTGAGGCCCTCTCCGTAAGCGGACCCAGAGTAAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGCTGCGTAAAGACATCATGCTCATCAAGTTGGACGAATCCGTGTCGAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGAGACATCAGCATTTGCTGCAAGTCCCTACCGCGGGGAATCTTCCCTC 339  
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTCTGGCTGGGCTGCTGCTGCGCAACGGTGAAGCTCAGGGGTGTGTGCTGCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
DB 400 AGAGGTCTCTGCGCAAGTCCGCGGGGCTGACCCAGACATCTGCTGCGTCCAGGCAATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCAAGTGC 477  
RESULT 13  
AR563667 1265 bp DNA linear PAT 08-OCT-2004  
LOCUS AR563667  
DEFINITION AR563667 Sequence 173 from patent US 6759515.  
ACCESSION AR563667  
VERSION AR563667.1 GI:53978718  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1265)  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Reiter, M.W., Stolk, J.A., Day, C.H., Vedelick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, M.T., and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6759515-A 173 06-JUL-2004;  
Corixa Corporation; Seattle, WA  
FEATURES  
source Location/Qualifiers  
1..1265  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores: 9,47e-65 Length: 1265  
Pred. No.: 758.00 Matches: 146  
Score: 100.0% Conservative: 0  
Percent Similarity: 100.0% Mismatches: 0  
Best Local Similarity: 100.0% Indels: 0  
Query Match: 2 Gaps: 0  
DB: 2  
US-10-726-093-10 (1-146) x AR563667 (1-1265)  
QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTyrValLeuSerAla 20  
DB 40 ATGGAAGAAACGAATTTGTTCTGCTCGGGCGCTCTGGTGATCCGACATGGGTGCTGACCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
DB 100 GCACACTGTTCCAGAACTCTACACATCGGGCTGGGCTGCACAGTCTTGAAGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyrAsn 60  
DB 160 CAAGAGCGCAGGAGACCGAGATGTTGAGGCCCTCTCCGTAAGCGGACCCAGAGTAAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGCTGCGTAAAGACATCATGCTCATCAAGTTGGACGAATCCGTGTCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGAGACATCAGCATTTGCTGCAAGTCCCTACCGCGGGGAATCTTGCCTC 339  
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120

Db 340 GTTCTGGCTGGGGTCTGCTGGCGAAGTGTCTACGGGTGTGTCTGCTTCTTCA 399  
QY 121 ATGATGSerSerAlaGlnSerArgGlyLeuThGlnSerSerAlaSerGlnAlaGluCys 140  
Db 400 AGAGAGTCTCTGCTGCTGGCGGGGAGCTGACCAAGTCTGTGCTCCAGGAGAAATGC 459  
QY 141 LeuProCysCysSerAla 146  
Db 460 CTACCGTGTGCTGAGTGGC 477  
RESULT 14  
ARS88653 1265 bp DNA linear PAT 15-DEC-2004  
LOCUS ARS88653  
DEFINITION Sequence 173 from patent US 6800746.  
ACCESSION ARS88653  
VERSION ARS88653.1 GI:56635550  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1265)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,  
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,  
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,  
Hepler,W.T. and Henderson,R.A.  
TITLES Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: US 6800746-A 173 05-OCT-2004;  
FEATURES  
source Corixa Corporation; Seattle, WA  
location/Qualifiers  
1..1265  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9,47e-65 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
DB: 2  
US-10-726-093-10 (1-146) x ARS88653 (1-1265)  
QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
Db 40 ATGAAACCAATTTGTTCTGCTGGGCTCTGCTGTCATCCGAGTGGGTGTCTGACCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
Db 100 GCACACTGTTTCCAGAACTCTACACCATGGGCTGGGCTGCACAGTCTTGAAGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyra 60  
Db 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCCAGCTCTCCCTACCGCACCCAGAGTCAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleTyrLeuAspGluSerValSerGluSer 80  
Db 220 AGACCTTGTCTGCTAAGCACTCATCTCATCAAGTTGAGCAAAATCCGTCCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
Db 280 GACACCATCCGAGCATCAGCATGCTTCCAGTGCCTACCCGCGGAGAACTCTGCTC 339  
QY 101 ValSerGlyTyrrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
Db 340 GTTTCGTGGGTGGGTCTGCTGGAGACGTGAGTCAAGGTGTGTCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThGlnSerSerAlaSerGlnAlaGluCys 140  
Db 400 AGAGAGTCTCTGCTGCTGGCGGGGAGCTGACCAAGTCTGTGCTCCAGGAGAAATGC 459

QY 141 LeuProCysCysSerAla 146  
Db 460 CTACCGTGTGCTGAGTGGC 477  
RESULT 15  
AR605473 1265 bp DNA linear PAT 15-DEC-2004  
LOCUS AR605473  
DEFINITION Sequence 173 from patent US 6818751.  
ACCESSION AR605473  
VERSION AR605473.1 GI:56657137  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1265)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,  
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,  
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,  
Hepler,W.T. and Henderson,R.A.  
TITLES Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: US 6818751-A 173 16-NOV-2004;  
FEATURES  
source Corixa Corporation; Seattle, WA  
location/Qualifiers  
1..1265  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9,47e-65 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
DB: 2  
US-10-726-093-10 (1-146) x AR605473 (1-1265)  
QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
Db 40 ATGAAACCAATTTGTTCTGCTGGGCTCTGCTGTCATCCGAGTGGGTGTCTGACCC 99  
QY 21 AlaHisCysPheGlnAsnSerTyThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
Db 100 GCACACTGTTTCCAGAACTCTACACCATGGGCTGGGCTGCACAGTCTTGAAGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTyra 60  
Db 160 CAAGAGCCAGGAGCCAGATGTGTGAGGCCAGCTCTCCCTACCGCACCCAGAGTCAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleTyrLeuAspGluSerValSerGluSer 80  
Db 220 AGACCTTGTCTGCTAAGCACTCATCTCATCAAGTTGAGCAAAATCCGTCCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
Db 280 GACACCATCCGAGCATCAGCATGCTTCCAGTGCCTACCCGCGGAGAACTCTGCTC 339  
QY 101 ValSerGlyTyrrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
Db 340 GTTTCGTGGGTGGGTCTGCTGGAGACGTGAGTCAAGGTGTGTCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThGlnSerSerAlaSerGlnAlaGluCys 140  
Db 400 AGAGAGTCTCTGCTGCTGGCGGGGAGCTGACCAAGTCTGTGCTCCAGGAGAAATGC 459  
Db 460 CTACCGTGTGCTGAGTGGC 477

Thu Aug 31 12:47:23 2006

us-10-726-093-10.rge

Page 9

Search completed: August 28, 2006, 19:37:59  
Job time : 3300 secs

---

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW protein - nucleic search, using frame\_plus.p2n model

Run on: August 28, 2006, 18:09:15 ; Search time 521 Seconds  
(without alignments)  
2930.753 Million cell updates/sec

Title: US-10-726-093-10  
Perfect score: 758  
Sequence: 1 MENELFCGVLVHPQWLSA.....SRGLTSSASQAELPCCSA 146

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5244920 seqs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+.p2n.model -DEV=xld  
-O=/absb/ABSSWB.spool/US10726093/runat\_28082006.121133\_25490/app.query.fasta\_1  
-DB=N.Geneseq -OFT=fastap -SUFPIX=ring -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -A:IGN=15 -MODE=LOCAL  
-OUTFMT=PLC -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03p  
-USER=US10726093 @CGN 1.1.1147 @runat\_28082006.121133\_25490 -NCPU=6 -ICPU=3  
-NO MMAP -NGC SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq.8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	100.0	702	4	AAC90119 Human pro
2	758	100.0	848	8	ABQ83341 Human KLK
3	758	100.0	1265	2	AAV58645 Prostate

4	758	100.0	1265	2	AAV61250 CDNA sequ
5	758	100.0	1265	3	AA06408 Human imm
6	758	100.0	1265	3	AB571313 Human pro
7	758	100.0	1265	4	AAH93524 Human pro
8	758	100.0	1265	4	AAH93524 Human pro
9	758	100.0	1265	4	AAH02589 Prostate
10	758	100.0	1265	4	AAH84838 Human pro
11	758	100.0	1265	5	ACAS9425 Prostate
12	758	100.0	1265	5	AAH84838 Human pro
13	758	100.0	1265	6	ABH94988 Human pro
14	758	100.0	1265	6	ABH94988 Human pro
15	758	100.0	1265	10	ACC95152 Prostate
16	758	100.0	1265	10	ADG326039 Human pro
17	758	100.0	1265	10	ADG326039 Human pro
18	758	100.0	1265	15	AEF66320 Human pro
19	758	100.0	1265	15	AEF66320 Human pro
20	660	87.1	4385	8	ABQ83347 Human KLK
21	660	87.1	4740	3	AAV58646 Prostate
22	660	84.4	1459	2	AAV58646 Prostate
23	640	84.4	1459	2	AAV61251 CDNA sequ
24	640	84.4	1459	3	AAH06409 Human imm
25	640	84.4	1459	3	AB571314 Human pro
26	640	84.4	1459	4	AAH93525 Human pro
27	640	84.4	1459	4	AAH02590 Prostate
28	640	84.4	1459	4	AAH84839 Human pro
29	640	84.4	1459	4	ACAS9426 Prostate
30	640	84.4	1459	5	AAH84839 Human pro
31	640	84.4	1459	5	AAH84839 Human pro
32	640	84.4	1459	6	ABH94989 Human pro
33	640	84.4	1459	6	ABH94989 Human pro
34	640	84.4	1459	10	ADG326040 Human pro
35	640	84.4	1459	10	ADG326040 Human pro
36	640	84.4	1459	15	AEF66321 Human pro
37	640	84.4	1459	15	AEF66321 Human pro
38	612	80.7	834	4	AAH90117 Human pro
39	612	80.7	834	4	AAH90117 Human pro
40	588	77.6	618	4	AAH90124 Human pro
41	588	77.6	618	4	AAH90124 Human pro
42	588	77.6	748	4	AAH93821 Human pro
43	588	77.6	765	4	AAH93821 Human pro
44	588	77.6	765	4	AAH63914 Human pro
45	588	77.6	765	4	AAH85135 Human pro

## ALIGNMENTS

RESULT 1	AAC90119	standard; cDNA; 702 BP.
ID	AAC90119	
XX	AAC90119	
AC		
XX		
XX		
DT	14-MAR-2001 (first entry)	
XX		
DE	Human prostate cancer-related intracellular protein CDNA #3.	
XX		
KW	Human; prostate cancer; intracellular protein; cytosolic; gene therapy;	
KW	breast cancer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200071711-A2.	
XX		
PD	30-NOV-2000.	
XX		
PF	19-MAY-2000; 2000MO-IB000673.	
XX		
PR	20-MAY-1999; 99US-0135325P.	
XX		
XX	20-MAY-1999; 99US-0135333P.	
PA	(SAAT/) SAATCIOGLU F.	
XX		
PI	Saatcioglu F;	

XX MPI; 2001-032036/04.  
DR P-PSDB; AAB50449.  
XX  
XX Novel nucleic acids encoding intracellular proteins useful for detecting  
PT neoplastic cell in a mammal, preferably the presence of prostate cancer  
or breast cancer.  
XX  
XX Claim 5; Page 17-18; 47pp; English.  
XX  
XX The present sequence encodes an intracellular protein which is  
CC differentially expressed in neoplastic cells, particularly prostate  
CC cancer cells. The polynucleotides and polypeptides are useful for  
CC diagnosing or detecting prostate cancer and breast cancer cells. The  
CC polynucleotides and polypeptides are also useful for treating cancer by  
CC antisense therapy and antibody based therapy, respectively.  
XX  
XX Sequence 702 BP; 135 A; 207 C; 213 G; 147 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 3.71e-70 Length: 702  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0  
US-10-726-093-10 (1-146) x AAC90119 (1-702)  
OY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
Db 1 ATGGAAGAAAGCAATGTTCTGCTCGGCGCTCTCGGCGCAATCCGACATGGGTCTGCACACC 60  
OY 21 AlaHisCysPheGlnAnSerSerThrTrpIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
Db 61 GCACACTGTTTCCAAACTCTCTACACCTCGGCTGGGCTGGGCTGCACAGCTTGAGGCCGAC 120  
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60  
Db 121 CAAGAGCCAGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTAACGCCACCCAGATACAAAC 180  
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnSer 80  
Db 181 AGACCTTGCTCGCTACAGACCTCACTGCTCACTCAAGATGGAGATCCGTGCTCGAGTCT 240  
OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
Db 241 GACACCATCCGAGCATCAAGCATTCCTGCGAGTCCCTTACCGCGGAGAACTCTTGCCCTC 300  
OY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120  
Db 301 GTTTCGTGCTGGGCGTCTGCTGCGAAGCGTGAAGCTCAGGGGTGTGTCTGCTGCTTCA 360  
OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlnCys 140  
Db 361 AGAGAGTCTCTCGCCAGTCCGGGGGCTGACCCAGCAAGCTCGCTCCAGGACAGAAATGC 420  
OY 141 LeuProCysCysSerAla 146  
Db 421 CTACCTGCTCTGAGTCCG 438  
RESULT 2  
ID ABO83341 standard; cDNA; 848 BP.  
XX ABO83341;  
AC ABO83341;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human KLK4 alternatively spliced variant encoding cDNA SEQ ID NO:1.  
XX  
KW Human; KLK4; cancer; benign tumour; cytostatic; variant; gene; ss.  
XX

OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 1.588  
FT CDS /\*tag= a  
FT /product= "KLK4 alternatively spliced variant"  
XX  
XX MO200277243-A1.  
XX  
XX 03-OCT-2002.  
XX  
XX 27-MAR-2002; 2002MO-AU000378.  
XX  
XX 27-MAR-2001; 2001AU-00004022.  
XX  
XX (UYOU-) UNIV QUEENSLAND TECHNOLOGY.  
XX  
XX Dong Y, Clements JA;  
XX  
XX MPI; 2003-029939/02.  
DR P-PSDB; ABP54355.  
XX  
XX Detecting the presence or diagnosing the risk of cancer or benign tumor,  
PT e.g. an ovarian, endometrial or prostate cancer, by determining the  
PT presence of or detecting aberrant expression of KLK4 in a biological  
PT sample from the patient.  
XX  
XX Claim 59; Page 106-107; 126pp; English.  
XX  
XX The present invention describes a method (M1) for detecting the presence  
CC or diagnosing the risk of cancer or benign tumor in a patient. M1  
CC comprises determining the presence of or detecting aberrant expression of  
CC KLK4 in a biological sample obtained from the patient. KLK4 has  
CC cytosolic activity. The method is useful for detecting the presence or  
CC diagnosing the risk of a cancer or a benign tumor in a patient,  
CC particularly an ovarian, endometrial or prostate cancer, or a cancer or  
CC benign tumor associated with an organ or tissue from the ovaries,  
CC endometrium or prostate. An agent which can be used for restoring or  
CC modulating KLK4 expression can be used for treating or preventing cancer  
CC or benign tumor. KLK4 polynucleotides, polypeptides or antigen-binding  
CC molecules from the present invention can be used for detecting aberrant  
CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a  
CC cancer or a benign tumor. The present sequence encodes a human KLK4  
CC alternatively spliced variant from the present invention.  
XX  
SQ Sequence 848 BP; 162 A; 254 C; 257 G; 175 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 4.8e-70 Length: 848  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0  
US-10-726-093-10 (1-146) x ABO83341 (1-848)  
OY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
Db 148 ATGGAAGAAAGCAATGTTCTGCTCGGCGCTCTCGGCGCAATCCGACATGGGTCTGCACACC 207  
OY 21 AlaHisCysPheGlnAnSerSerThrTrpIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
Db 208 GCACACTGTTTCCAAACTCTCTACACCTCGGCTGGGCTGGGCTGCACAGCTTGAGGCCGAC 267  
OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60  
Db 268 CAAGAGCCAGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTAACGCCACCCAGATACAAAC 327  
OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnSer 80  
Db 328 AGACCTTGCTCGCTACAGACCTCACTGCTCACTCAAGATGGAGATCCGTGCTCGAGTCT 387

Qy	81	AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaIleValAsnSerCysLeu	100
Db	388	GACACCATCCGGAGCATCAGCATTCCTTCGCAGTCCCTACCGCGGGAACTCTTGCTC	447
Qy	101	ValSerGlyThrGlyIleuLeuAlaAsnGlyIleuThrGlyValCysLeuProSerSer	120
Db	448	GTTCTGGCTGGGGGTCTGCTGGCGAAAGGTAGCTCAGGGGTGTGTCTGCCCTTTCA	507
Qy	121	ArgArgSerSerAlaGlnSerArgGlyIleuThrGlnSerSerAlaSerGlnAlaGluCys	140
Db	508	AGGAGGTCTCTCTCCAGTCCGCGGGGCTGACCCAGAGCTCTGCTCCACGAGAAATGC	567
Qy	141	LeuProCysCysSerAla 146	
Db	568	CTACCGTCTGCAGTGC 585	
RESULT 3			
ID	AAV58645		
ID	AAV58645	standard; cDNA; 1265 BP.	
XX	AAV58645;		
AC			
XX	AAV58645;		
DT	25-MAR-2003	(revised)	
DT	08-DEC-1998	(first entry)	
XX			
DE	Prostate tumour specific gene clone DE2.		
XX			
KW	Prostate tumour specific gene; human; prostate cancer; detection;		
XX	therapy; ss.		
OS	Homo sapiens.		
XX			
XX	WO9837418-A2.		
PN			
PD	27-AUG-1998.		
XX			
PF	25-FEB-1998;	98MO-US003690.	
XX			
PR	25-FEB-1997;	97US-008064596.	
XX	01-AUG-1997;	97US-00804809.	
PR	09-FEB-1998;	98US-00020747.	
XX			
PA	(CORI-) CORIXA CORP.		
XX			
XX	Xu J, Dillon DC;		
PI			
XX	WPI; 1998-480805/41.		
DR			
PT	Novel human prostate specific tumour protein and fragments - useful for		
XX	detecting and treating prostate cancers.		
PS	Claim 1; Page 113-114; 141pp; English.		
XX			
CC	This sequence represents a human prostate tumour specific gene, and can		
XX	be used in the method of the invention. The method is for detecting		
CC	prostate cancer comprises contacting a biological sample with an agent		
XX	able to bind an immunogenic portion of a prostate protein (such as		
CC	encoded by this sequence). An antibody which binds to an immunogenic		
XX	portion of the prostate protein, and the method can be used to detect,		
CC	monitor progression of, or treat prostate cancers. The antibody may also		
XX	be conjugated to a therapeutic agent for use in therapy of prostate		
CC	cancers. (Updated on 25-MAR-2003 to correct PR field.)		
XX			
SO	Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;		
Alignment Scores:			
Pred. No.:	8,296-70	Length:	1265
Score:	758.00	Matches:	146
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-726-093-10 (1-146) x AAV58645 (1-1265)

QY 1 MetGlnaSnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
Db 40 ATGGAAACCAATGTCTCTGCTCGGGCGCTCTGGTGCATCCGACGTGGGTCTGTCAGCC 99  
QY 21 AlaHisCysPheGlnaSnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
Db 100 GCACACAGTGTCCAGAACTCTTACACCATCGGGCTGGGCTTCGACACGTCTTGAAGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValAlaArgHisProGluTyrAsn 60  
Db 160 CAAAGCCCAAGGAGCAGCAGATGATGGAGCCAGCCTTCGGTACGGCACCAGACTACAAAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
Db 220 AGACCTTGTGCTCGCTACGACCTCATCTCATCTCAATGAGCGAATCCGTGTCCGAGTCT 279  
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
Db 280 GACACCAATCCGAGACATCAGCATTCCTTCGACAGTCCCTACCGGGGGAACTTTGGCTTC 339  
QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
Db 340 GTTCTGGCTGGGTCTGCTGGCGACAGGTGAGCTCACGGGTGTTGTCTGCTCCCTTTCAC 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
Db 400 AGGAGGTCTCTGCGCCAGTCCGCGGGGGCTGACCCAGAGCTCTGCGTCCCAAGACAAATGC 459  
QY 141 LeuProCysCysSerAla 146  
Db 460 CTACCGTGTCTCAAGTGC 477

RESULT 4  
AAV61250  
ID AAV61250 standard: cDNA, 1265 BP.  
XX AAV61250;  
AC AAV61250;  
XX  
DT 06-JAN-1999 (first entry)  
XX  
DE cDNA sequence of prostate tumour clone P703 splice variant DE2.  
XX  
KM Prostate; cancer; tumour; vaccine; immunogen; clone; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9837093-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 25-FEB-1998; 98WO-US003492.  
XX  
PR 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 09-FEB-1998; 98US-00020956.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Dillon DC;  
XX  
DR WPI; 1998-609886/51.  
XX  
PT Polyepitides comprising immunogenic portions of prostate proteins - used  
XX in a vaccine for the treatment of prostate cancer.  
XX  
PS Claim 3; Page 105-106; 130pp; English.  
XX  
CC The present sequence is a new DNA which encodes an immunogenic portion of  
CC a prostate tumour protein. The encoded immunogen, or the DNA itself, can  
CC be used as a vaccine for the treatment of prostate cancer. The DNA was  
CC identified by analysis of a subtracted cDNA library obtained by



AB571313  
ID AB571313 standard; cDNA; 1265 BP.  
XX  
AC AB571313;  
XX  
DT 27-NOV-2002 (first entry)  
XX  
DE Human prostate tumour protein partial DNA sequence #163.  
XX  
KW Human; immunogenic; prostate protein; prostate tumour protein;  
XX  
KM prostate cancer; cytostatic; vaccine; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002090372-A1.  
PD 11-JUL-2002.  
XX  
PF 14-JUL-1998; 98US-00115453.  
XX  
PR 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 09-FEB-1998; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
XX  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PI Xu J, Dillon DC;  
XX  
DR WPI; 2000-171268/15.  
XX  
PT New polypeptide useful for treating and diagnosing prostate cancer  
XX  
PT comprises an immunogenic portion of prostate tumor protein.  
XX  
PS Claim 3; Page 78-79; 101pp; English.  
XX  
CC The present invention relates to a new polypeptide comprising an  
XX  
CC immunogenic portion of a prostate protein. The invention is useful for  
XX  
CC inhibiting the development of prostate cancer in a patient. The invention  
XX  
CC is also useful as markers for diagnosing prostate cancer and for  
XX  
CC monitoring diseases progression in patients. The present nucleic acid  
XX  
CC sequence represents a DNA sequence that is part of a gene encoding a  
XX  
CC human prostate tumour protein  
XX  
SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;  
Alignment Scores:  
Pred. No.: 8.29e-70 Length: 1265  
Score: 758.00 Matches: 146  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
US-10-726-093-10 (1-146) x AB571313 (1-1265)  
QY 1 MetGlaAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
DB 40 ATGGAAGAACAAATTGTTCTCTCGGGCGTCTGTCGATCCGACAGTGGGCTGTCAGCC 99  
QY 21 ALAHISCySPheGlnAsnSerYrTrhIleGlyLeuGlyLeuHisSerLeuGluAlaASP 40  
DB 100 GCACACGTGTTCCAGAACTCTACACCATCGGGCTGGGCTTGACAGTCTTGAGGCCGAC 159  
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpValAsn 60  
DB 160 CAAGAGCGAGGAGCCAGATGGTGGAGCCAGCTCTCCGACGGACCCAGAGTACAC 219  
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleYsLeuAspGluSerValSerGluSer 80  
DB 220 AGACCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGACGAATCGGTCCGAGTCT 279

QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
DB 280 GACACCATCCGGAGCATCAGCAATTGCTTCGACAGCCCTACCGGGGGAACCTTGCTC 339  
QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGlyLeuThrGlyValCysLeuProSerSer 120  
DB 340 GTTCTGCTGGGGGTGCTGCGACACGGTGAAGCTCACGGGTGTGTCTGCTCTTCA 399  
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140  
DB 400 AGGAGGTCTCTTCCAGTCCGGGGGGGTGACCCAGAGCTTGTGCTCCAGGCAAAATGC 459  
QY 141 LeuProCysCysSerAla 146  
DB 460 CTACCGTCTGCTCACTGCG 477  
RESULT 7  
AAH93524  
ID AAH93524 standard; cDNA; 1265 BP.  
XX  
AC AAH93524;  
XX  
DT 04-OCT-2001 (first entry)  
XX  
DE Human prostate-specific cDNA sequence P703P-DE2.  
XX  
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
XX  
KM cytostatic; gene therapy; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200151633-A2.  
XX  
PD 19-JUL-2001.  
XX  
PF 16-JAN-2001; 2001WO-US001574.  
XX  
PR 14-JAN-2000; 2000US-00483672.  
XX  
PA (CORI-) CORIAX CORP.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,  
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;  
PI Wang A, Meagher MJ;  
XX  
DR WPI; 2001-425873/45.  
XX  
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,  
XX  
PT monitoring and treating prostate cancer in a patient and for use in  
XX  
PT vaccines.  
XX  
PS Claim 1; Page 285-286; 543pp; English.  
XX  
CC The present invention describes polynucleotide sequences (I) which encode  
XX  
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
XX  
CC and can be used in vaccine production and gene therapy. (I), (II),  
XX  
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells  
XX  
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and  
XX  
CC the antibodies are also used in the detection of cancer in a patient. The  
XX  
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)  
XX  
CC and (II) can be used in vaccines. The antibodies or (I) and (II) can be  
XX  
CC monitoring the progression of cancer in a patient. (I) and (II) can also  
XX  
CC be used to improve diagnostic and therapeutic methods for prostate  
XX  
CC cancer. They can indicate the level of metastasis as well as the prostate  
XX  
CC volume. AAH93524 to AAH93944 and AAH01115 to AAH01318 represent  
XX  
CC polynucleotide and amino acid sequences used in the exemplification of  
XX  
CC the present invention  
XX  
SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;  
Alignment Scores:  
Pred. No.: 8.29e-70 Length: 1265  
Score: 758.00 Matches: 146



Percent Similarity: 100.0%  
 Best Local Similarity: 100.0%  
 Query Match: 100.0%  
 Gaps: 4  
 Indels: 0  
 Mismatches: 0  
 Conservative: 0

US-10-726-093-10 (1-146) x AAH93524 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTyrValLeuSerAla 20  
 DB 40 ATGGAAAACGATTTCTTCGCTCGGGCGTCTCGGTGCATCCGACAGTGGCTGCTGCACCC 99  
 QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
 DB 100 GCACACTCTTTCCACAACTCTTACACCACTCGGGCTGGGCTGCACAGCTTGAGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60  
 DB 160 CAAGAGCCAGGAGGACCAATGTTGGAGGCCAGCTCTCTCGTACGGACCCAGAGTACAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleGlyLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGTCTCGTAAACGACTCATCTCAATGAGAGCAATCCGTGCGAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCAATCCGAGAGCATGAGCATTTCTTGCAGTCCCTACCGCGGGAACCTTGTGCTC 339  
 QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTCTGTGCTGGGCTCTCTGCTGCGAAGCTGAGCTCAGGGTGTGTCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGGAGGTCTCTGCGCCAGTGGCGGGGCTGACCCAGAGCTCTGCTGCCAGGACGAATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTGTGCAATGCG 477

RESULT 8

AAH02589 ID AAH02589 standard; cDNA, 1265 BP.

AAH02589 AC AAH02589 standard; cDNA, 1265 BP.

AAH02589 DT 29-JAN-2002 (first entry)

AAH02589 DE Human prostate cDNA sequence #168.

AAH02589 KW Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.

AAH02589 OS Homo sapiens.

AAH02589 PN WO200173032-A2.

AAH02589 PD 04-OCT-2001.

AAH02589 PF 27-MAR-2001; 2001WO-US009919.

AAH02589 PR 27-MAR-2000; 2000US-00516857.

AAH02589 PR 09-MAY-2000; 2000US-00588100.

AAH02589 PR 12-MAY-2000; 2000US-00570737.

AAH02589 PR 13-JUN-2000; 2000US-00593793.

AAH02589 PR 27-JUN-2000; 2000US-00605783.

AAH02589 PR 09-AUG-2000; 2000US-00636215.

AAH02589 PR 29-AUG-2000; 2000US-00651236.

AAH02589 PR 06-SEP-2000; 2000US-00657279.

AAH02589 PR 02-OCT-2000; 2000US-00679426.

AAH02589 PR 10-OCT-2000; 2000US-00685166.

AAH02589 PR 09-NOV-2000; 2000US-00709729.

AAH02589 PA (CORI-) CORIXA CORP.

AAH02589 XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
 PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;  
 XX  
 DR WPI: 2001-639232/73.

PT New human prostate-specific polypeptides and polynucleotides useful for  
 PT the diagnosis and treatment of cancer, especially prostate cancer.

PS Claim 1; Page 287; 579pp; English.

XX  
 CC The invention relates to isolated prostate-specific polynucleotides,  
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised  
 CC against the polypeptides (or antigenic epitopes derived from them) and  
 CC antigen-presenting cells expressing the polypeptides. The antibodies are  
 CC useful for detecting the presence of cancer, especially prostate cancer.  
 CC The polypeptides, polynucleotides and the antigen-presenting cells are  
 CC useful for stimulating and/or expanding T cells specific for a tumour  
 CC protein, and for inhibiting the development of cancer especially prostate  
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are  
 CC useful for stimulating an immune response, and for treating cancer. The  
 CC oligonucleotide is useful for detecting cancer. The present sequence is a  
 CC prostate specific polynucleotide of the invention

SO Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.: 8,296-70 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 4 Gaps: 0

US-10-726-093-10 (1-146) x AAH02589 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTyrValLeuSerAla 20  
 DB 40 ATGGAAAACGATTTCTTCGCTCGGGCGTCTCGGTGCATCCGACAGTGGCTGCTGCACCC 99  
 QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
 DB 100 GCACACTCTTTCCACAACTCTTACACCACTCGGGCTGGGCTGCACAGTCTTGAGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60  
 DB 160 CAAGAGCCAGGAGGACCAATGTTGGAGGCCAGCTCTCTCGTACGGACCCAGAGTACAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleGlyLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGTCTCGTAAACGACTCATCTCAATGAGAGCAATCCGTGCTCGAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCAATCCGAGAGCATGAGCATTTCTTCCAGAGCCCTACCGGGGAACCTTGTGCTC 339  
 QY 101 ValSerGlyTyrGlyLeuLeuAlaAsnGlyLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTCTGTGCTGGGCTCTGCTGCGAAGCTGAGCTCAGGGTGTGTCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGGAGGTCTCTGCGCCAGTGGCGGGGCTGACCCAGAGCTCTGCTGCCAGGACGAATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTGTGCAATGCG 477

RESULT 9

AAH02589 ID AAH02589 standard; cDNA, 1265 BP.

AAH02589 AC AAH02589 standard; cDNA, 1265 BP.

XX 14-JUN-2001 (first entry)  
 DT Prostate tumour antigen determined cDNA sequence for P703P-DE2.  
 XX  
 DE Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;  
 XX prostate cancer; immunogenic; cytostatic; vaccine; ss.  
 KW Homo sapiens.  
 XX  
 OS WO200152272-A2.  
 PN 12-APR-2001.  
 PD 04-OCT-2000; 2000WO-US027464.  
 PF 04-OCT-1999; 99US-0157455P.  
 PR 04-OCT-1999; 99US-0157455P.  
 XX (CORI-) CORIXA CORP.  
 XX  
 PA Xu J, Skeiky YAW, Reed SG, Cheever MA;  
 PI WPI, 2001-245062/25.  
 DR  
 XX Prostate specific protein and its encoding polynucleotide, useful for the  
 PT treatment and diagnosis of prostate cancer.  
 PT  
 XX Claim 4; Page 174; 276pp; English.  
 PS  
 XX The present invention describes an isolated polypeptide (I) comprising at  
 CC least an immunogenic portion of a prostate tumour antigen protein or its  
 CC variant. (I) have cytostatic activity and can be used in vaccine  
 CC production. (I), prostate tumour antigen polynucleotides, an antigen  
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a  
 CC pharmaceutical composition containing (I) are useful for inhibiting the  
 CC development of cancer in a patient. Antibodies specific for prostate  
 CC specific proteins and oligonucleotides that hybridise to a polynucleotide  
 CC that encodes a prostate specific protein are useful for detecting the  
 CC presence or absence of a cancer or monitoring the progression the  
 CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,  
 CC AAH74798 to AAH74821 and AAH74830 are sequences used in the  
 CC exemplification of the present invention  
 CC  
 CC  
 SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:  
 Pred. No.: 8.29e-70 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 4 Gaps: 0

US-10-726-093-10 (1-146) x AAH02589 (1-1265)

QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAAGAACCAATTGTTCTGCTGGGGCGTCTGGTGATCCGACGTGGGTGCTGACGCC 99  
 QY 21 AlHisCysPheGlnAsnSerTYrThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
 DB 100 GCACACTGTTCCGAACCTCTACACCATCGGGCTGGCCCTGCACAGTCTTGAAGCCGAC 159  
 QY 41 GlnGluPProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTrpAsn 60  
 DB 160 CAAGAGCCAGGAGCCGAGATGTGTGAAGCCAGCTCTCCGACCGCACCCAGAGTACAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGlnSerValSerGlnSer 80  
 DB 220 AGACCTTGTCTCGCTAAGCATCTCATCAAGTTGACGAGATCCGTCTCCGAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlnAsnSerCysLeu 100

DB 280 GACACCATCCGAGCATCAGCATGCTTCGCGAGTCCCTACCGCGGGGAACTTTCCTC 339  
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTCTGCTGGGGTCTGCTGGTCCGACGAGTGCACAGGGTGTGTCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGGAGTCTCTGCTGCCACTCCGCGGGGCTGACCCAGAGCTCTGGCTCCAGGCAAGATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTCTGCAAGTGC 477

RESULT 10  
 AAH84838  
 ID AAH84838 standard; cDNA; 1265 BP.  
 XX  
 AC AAH84838;  
 XX  
 DT 25-SEP-2001 (first entry)  
 XX  
 DE Human prostate-specific cDNA sequence P703P-DE2.  
 XX  
 KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;  
 KW chromosome 22q11.2; prostate-specific protein; chromosome 1;  
 KW prostate specific antigen; PSA; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200134802-A2.  
 PD 17-MAY-2001.  
 PF 09-NOV-2000; 2000WO-US030904.  
 XX  
 PR 12-NOV-1999; 99US-00439313.  
 PR 18-NOV-1999; 99US-00443666.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PI  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
 PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;  
 XX WPI, 2001-308785/32.  
 DR  
 XX Isolated polypeptide comprising at least an immunogenic portion of a  
 PT prostate-specific protein, useful in the diagnosis and therapy of a  
 PT prostate cancer.  
 PS Claim 5; Page 185; 325pp; English.  
 XX  
 XX The present invention describes an isolated polypeptide (P1) comprising  
 CC at least an immunogenic portion of a prostate-specific protein, or its  
 CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and  
 CC (N1) have cytostatic activity and can be used in vaccine production. The  
 CC polypeptides, nucleic acids and antibodies from the present invention are  
 CC useful in the diagnosis and therapy of prostate cancer. Prostate specific  
 CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic  
 CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.  
 CC Prostate specific antigen (PSA) P501S was located on chromosome 1.  
 CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide  
 CC and polypeptide sequences used in the exemplification of the present  
 CC invention  
 CC  
 CC  
 SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:  
 Pred. No.: 8.29e-70 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0

```

DB: 4 Gaps: 0
US-10-726-093-10 (1-146) x AAH84838 (1-1265)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTTPValLeuSerAla 20
DB 40 ATGGAAACGAATTGTTCTGCTCGGCGCTGCTGCGATCCGACATGGGTGCTGTCAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaSP 40
DB 100 GCACACTGTTTCCAAACTCCCTACACCATCGGCGCTGGCGCTGCACAGTCTTGAGGCCAG 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGCTGAGGCGCAGCTCTCCGTACCGCACCCAGAGTACAAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTACACCACTCATGCTCATGAGTGGACGAATCCGTGTCCAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 CACACCAATCCGAGCATACGATTCCTTCCAGTCCCTACCGCGGGAACCTTGCTTC 339
QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
DB 340 GTTCTGGCTGGGCTGCTGCTGCGAAACGGTGAAGCTCAGCGGTGTGTCTGCTCTTCA 399
QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140
DB 400 AGGAGGTCTCTGCGCCAGTCGGGGGGCTGACCCAGACTCTGCTGCCAGGACGAATGC 459
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCTGCTGCAATGCC 477
QY 141 LeuProCysCysSerAla 146
DB 460 CTACCTGCTGCAATGCC 477
RESULT 11
ID ACAS9425
ID ACAS9425 standard; cDNA; 1265 BP.
AC ACAS9425;
AC ACAS9425;
DT 10-JUN-2003 (first entry)
XX XX
DE Prostate cancer therapy associated cDNA #168.
XX XX
KM Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KM immunogen; cancer; prostate specific antigen; PSA;
KM prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KM PSMA; gene; ss.
XX XX
OS Homo sapiens.
XX XX
PN US2002192763-A1.
XX XX
PD 19-DEC-2002.
XX XX
PF 29-JUN-2001; 2001US-00895793.
XX XX
PR 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARU/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) BETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.

```

```

PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (BAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX XX
DR WPI; 2001-245062/25.
XX XX
PT Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX XX
PS Example 3; SEQ ID NO 173; 65pp; English.
XX XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences; not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?docid=US20020192763
CC XX
SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;
XX XX
Alignment Scores:
Pred. No.: 8 298-70 Length: 1265
Score: 758.00 Matches: 146
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0
US-10-726-093-10 (1-146) x ACAS9425 (1-1265)
QY 1 MetGluAnGluLeuPheCysSerGlyValLeuValHisProGlnTTPValLeuSerAla 20
DB 40 ATGGAAACGAATTGTTCTGCTCGGCGCTGCTGCGATCCGACATGGGTGCTGTCAGCC 99
QY 21 AlaHisCysPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaSP 40
DB 100 GCACACTGTTTCCAAACTCCCTACACCATCGGCGCTGGCGCTGCACAGTCTTGAGGCCAG 159
QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60
DB 160 CAAGAGCCAGGAGCCAGATGCTGAGGCGCAGCTCTCCGTACCGCACCCAGAGTACAAAC 219
QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
DB 220 AGACCTTGCTGCTACACCACTCATGCTCATGAGTGGACGAATCCGTGTCCAGTCT 279
QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
DB 280 GACACCAATCCGAGCATACGATTCCTTCCAGTGGCTTACCGGGGAACCTTGCTTC 339
QY 101 ValSerGlyTTPGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120

```

```
Db      340 GTTCTGCTGGGCTCTGCTGGCGAAGCTGAGCTCAGCGGTGTGTCTGCCCTCTTCA 399
Oy      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140
Db      400 AGAGAGTCTCTGCTGCCAGTCGGGGGGCTGACCCAGAGCTGCTGCCAGGAGAAATGC 459
Oy      141 LeuProCysCysSerAla 146
Db      460 CTACCGTCTGTCAGTGC 477

RESULT 12
AAS10167
ID      AAS10167 standard; cDNA; 1265 BP.
XX      AAS10167;
XX      AAS10167;
XX      24-OCT-2001 (first entry)
XX      Human prostate tumour CDNA DE2.
XX      Human prostate tumour protein; prostate cancer; ss.
XX      Homo sapiens.
XX      US6262245-B1.
XX      17-JUL-2001.
XX      PD
XX      PF 25-FEB-1998; 98US-00030607.
XX      PR 25-FEB-1997; 97US-00806099.
XX      PR 01-AUG-1997; 97US-00904804.
XX      PR 09-FEB-1998; 98US-00020956.
XX      PA (CORI-) CORIXA CORP.
XX      PI Xu J, Dillon DC;
XX      DR WPI, 2001-440862/47.
XX      CC Novel polynucleotide encoding polypeptide comprising a portion of
XX      PT prostate tumor protein useful for inhibiting development of prostate
XX      PT cancer or for treating prostate cancer in a patient.
XX      PS Example 2; Col 169; 105pp; English.
XX      CC The sequence is a human prostate tumour CDNA which encodes a partial
XX      CC tumour protein. The DNA is useful for inhibiting the development of
XX      CC prostate cancer or for treating prostate cancer in a patient
XX      SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Alignment Scores:
Pred. No.:      8 296-70      Length:      1265
Score:          758.00      Matches:      146
Percent Similarity: 100.0%      Mismatches: 0
Best Local Similarity: 100.0%      Indels:      0
Query Match:      5          Gaps:      0

US-10-726-093-10 (1-146) x AAS10167 (1-1265)
Oy      1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20
Db      40 ATGGAAAGCAATGTTCTGCTCGGGCGTCTGTGTCATCCGAGTGGGTGCTGTCAGCC 99
Oy      21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40
Db      100 GCACACTGTTTCCAGAACTCTACACCATCGGGCTGGCTGCAGCTCTTAGAGCGGAC 159
Oy      41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60
Db      160 CAAGAGCCAGGAGGACGATGTGGAGGCCAGCTCTCCGTACGGCACCAGAGTAAAC 219
```

```
Oy      61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLysLeuAspGluSerValSerGluSer 80
Db      220 AGACCTTGTCTGCTCAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCAGACT 279
Oy      81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100
Db      280 GACACATCCGGAGCATCAGCATGCTTCCGAGTCCCTACCGCGGGAACTCTTGCTTC 339
Oy      101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120
Db      340 GTTCTGCTGGGCTGCTGCTGCGAAGCTGAGCTCAGGGGTGTGTCTGCCCTCTTCA 399
Oy      121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGlyCys 140
Db      400 AGAGAGTCTCTGCTGCCAGTCGGGGGGCTGACCCAGAGCTCTGCTGCCAGGAAATGC 459
Oy      141 LeuProCysCysSerAla 146
Db      460 CTACCGTCTGTCAGTGC 477

RESULT 13
ABL94988
ID      ABL94988 standard; cDNA; 1265 BP.
XX      ABL94988;
XX      AC
XX      AC 19-JUL-2002 (first entry)
XX      DT
XX      DE Human P703P-DE2 CDNA sequence SEQ ID NO 173.
XX      DE Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX      KM gene therapy; gene; ss.
XX      OS Homo sapiens.
XX      PN US2002022248-A1.
XX      PD 21-FEB-2002.
XX      PF 12-JAN-2001; 2001US-00759143.
XX      PR 25-FEB-1997; 97US-00806099.
XX      PR 01-AUG-1997; 97US-00904804.
XX      PR 10-FEB-1998; 98US-00020956.
XX      PR 25-FEB-1998; 98US-00030607.
XX      PR 14-JUL-1998; 98US-00115453.
XX      PR 23-SEP-1998; 98US-00159812.
XX      PR 15-JAN-1999; 99US-00232149.
XX      PR 09-APR-1999; 99US-00288946.
XX      PR 13-JUL-1999; 99US-00352616.
XX      PR 12-NOV-1999; 99US-00439313.
XX      PR 18-NOV-1999; 99US-00443686.
XX      PR 14-JAN-2000; 2000US-00483672.
XX      PR 27-MAR-2000; 2000US-00536857.
XX      PR 09-MAY-2000; 2000US-00568100.
XX      PR 12-MAY-2000; 2000US-00570737.
XX      PR 13-JUN-2000; 2000US-00583793.
XX      PR 27-JUN-2000; 2000US-00605783.
XX      PR 10-AUG-2000; 2000US-00636215.
XX      PR 29-AUG-2000; 2000US-00651236.
XX      PR 06-SEP-2000; 2000US-00657279.
XX      PR 02-OCT-2000; 2000US-00679426.
XX      PR 10-OCT-2000; 2000US-00685166.
XX      PA (XUJ/) XU J.
XX      PA (DILL/) DILLON D C.
XX      PA (MITCH/) MITCHAM J L.
XX      PA (HARL/) HARLOCKER S L.
XX      PA (JIAN/) JIANG Y.
XX      PA (KALO/) KALOS M D.
XX      PA (FANG/) FANGER G R.
XX      PA (RETT/) RETTER M W.
```

PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
 XX  
 DR WPI; 2002-255649/30.  
 XX  
 PT New prostate-specific polynucleotides for diagnosing and treating  
 PT diseases, in particular prostate cancer, and as markers for the  
 PT progression of cancer.  
 XX  
 PS Claim 1; SEQ ID NO 173; 87bp; English.  
 XX  
 CC The present invention provides prostate-specific coding sequences and  
 CC their encoded proteins. These can be used in the diagnosis and treatment  
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA  
 CC described in the invention  
 XX  
 SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;  
 Alignment Scores:  
 Pred. No.: 8,29e-70 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: Gaps: 0  
 US-10-726-093-10 (1-146) x ABL94988 (1-1265)  
 OY 1 MetGluAnGluLeuPheCySerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAAGAAAGATTGTTCTGCTCGGGCGCTCGTGCAATCCGACATGGGTCTGTCAAGCC 99  
 OY 21 AlaHisCySPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40  
 DB 100 GCACACTGTTCCAGAACTCTACACCAATCGGGCTGGCGCTCCACAGTCTTAGCGCCGAC 159  
 OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60  
 DB 160 CAAGAGCCAGGAGGAGATGATGTGAGGCGACCTCTCCGTACGGACCCAGAGTACAAAC 219  
 OY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleLeuValAspGluSerValSerGluSer 80  
 DB 220 AGACCTTGCTGCTGTAACGACTCACTCATCAAGTTGAGAGAAATCCGTGCCAGTCT 279  
 OY 81 AspThrIleArgSerIleSerIleAlaSerGlnCySProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCATCCGAGAGCATCAGCATGCTTCGACATGCCCTACCGCGGGAACCTTGGCCTC 339  
 OY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyValLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTTCGGGTGGGGTGTGCTGGGAGAGGTGAGCTTACCGGGTGTGTGCTGCCCTCTTCA 399  
 OY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGAGAGTCTCTGCCAGTCGGGGGGGTGACCCAGAGCTTGGCGTCCAGGACAGAAATGC 459  
 OY 141 LeuProCySCysSerAla 146  
 DB 460 CTACCGTCTGCAGTCCG 477  
 RESULT 14  
 ABS58697

ID ABS58697 standard; cDNA; 1265 BP.  
 XX  
 AC ABS58697;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Prostate tumour cDNA #168.  
 XX  
 KW Human; prostate tumour; immunotherapy; prostate cancer; gene; ss.  
 OS Homo sapiens.  
 XX  
 XX US2002081580-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 XX 25-FEB-1998; 98US-00030606.  
 XX  
 XX 25-FEB-1997; 97US-00806596.  
 XX  
 PR 01-AUG-1997; 97US-00904809.  
 PR  
 PR 09-FEB-1998; 98US-00020747.  
 XX  
 XX (XUJ/) XU J.  
 PA (DILL/) DILLON D C.  
 XX  
 PI Xu J, Dillon DC;  
 XX  
 DR WPI; 2002-607662/65.  
 XX  
 PT Detecting prostate cancer comprises contacting a sample with an agent  
 PT capable of binding to a polypeptide with an immunogenic portion of a  
 PT prostate protein, oligonucleotide primers or a probe specific for DNA  
 PT encoding the polypeptide.  
 XX  
 XX Example 3; Page 88-89; 111pp; English.  
 XX  
 CC The invention relates to a method of detecting prostate cancer by  
 CC contacting a biological sample from a patient with: (a) a binding agent  
 CC that binds to a polypeptide having an immunogenic portion of a prostate  
 CC protein or its variant; (b) 2 oligonucleotide primers, where 1 of the  
 CC oligonucleotides is specific for a DNA encoding the polypeptide of (a);  
 CC or (c) an oligonucleotide probe specific for a DNA molecule encoding the  
 CC polypeptide of (a). The method and polypeptides are useful for  
 CC diagnosing, treating, particularly by immunotherapy, monitoring the  
 CC progression, and inhibiting the development of prostate cancer in a  
 CC patient. The polypeptides may be used to generate antibodies useful for  
 CC the diagnosis and monitoring of prostate cancer. ABS58530-ABS58746  
 CC represent human prostate tumour cDNA sequences of the invention  
 XX  
 SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;  
 Alignment Scores:  
 Pred. No.: 8,29e-70 Length: 1265  
 Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: Gaps: 0  
 US-10-726-093-10 (1-146) x ABS58697 (1-1265)  
 OY 1 MetGluAnGluLeuPheCySerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAAGAAAGATTGTTCTGCTCGGGCGCTCGTGCAATCCGACATGGGTCTGTCAAGCC 99  
 OY 21 AlaHisCySPheGlnAsnSerTyrThrIleGlyLeuGlyLeuHisSerLeuGluAlaasp 40  
 DB 100 GCACACTGTTCCAGAACTCTACACCAATCGGGCTGGCGCTCCACAGTCTTAGAGCCGAC 159  
 OY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGlnTyrAsn 60  
 DB 160 CAAGAGCCAGGAGGAGATGATGTGAGGCGACCTCTCCGTACGGACCCAGAGTACAAAC 219

QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCCCTTCCTCGCTACACCTCATGCTCATCAAGTTGAGCAATCCCTGTCGGAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCATCCGAGCATCGACTGCTGTCAGTCCCTACCGCGGGGAACTCTTGCTTC 339  
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTTCGCTGCGGCTGCTGCTGCGAAGCGTGAAGTCAACGGGTGTGTCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGAGAGTCTCTGCTGCCAGTCCGCGGGGCTGACCCAGAGCTGCTGCCAGCAGCAATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTCTGCTGAGTCCG 477  
 RESULT 15  
 ACC95152  
 ID ACC95152 standard; cDNA; 1265 BP.  
 AC ACC95152;  
 XX  
 DT 28-AUG-2003 (first entry)  
 XX  
 DE Prostate tumour specific cDNA sequence SEQ ID 173.  
 XX  
 KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;  
 XX  
 OS Immune response; prostate cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200289747-A2.  
 PD 14-NOV-2002.  
 PF 09-MAY-2002; 2002MO-US014753.  
 XX  
 XX 09-MAY-2001; 2001US-00852911.  
 PR 29-JUN-2001; 2001US-00895814.  
 PR 10-DEC-2001; 2001US-00012896.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;  
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
 PI McNeill PD, Houghon RL, Vinals Y De Bassols, Foy TW, Watanabe Y;  
 PI Deng T;  
 XX  
 DR WPI; 2003-167130/16.  
 XX  
 PT New prostate-specific proteins and genes, useful in gene therapy,  
 PT particularly for stimulating an immune response in a patient, or treating  
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer  
 PT in a patient.  
 XX  
 PS Example 3; Page 353; 691pp; English.  
 XX  
 PS The present invention relates to novel prostate-specific proteins (PSP)  
 CC and their coding sequences. The PSPs and their coding sequences are  
 CC useful for stimulating an immune response in a patient, or for treating  
 CC prostate cancer in a patient and for determining, detecting or diagnosing  
 CC the presence of a cancer in a patient. The present sequence was used to  
 CC illustrate the invention  
 XX  
 SQ Sequence 1265 BP; 256 A; 432 C; 321 G; 245 T; 0 U; 11 Other;

Score: 758.00 Matches: 146  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-726-093-10 (1-146) x ACC95152 (1-1265)  
 QY 1 MetGluAsnGluLeuPheCysSerGlyValLeuValHisProGlnTrpValLeuSerAla 20  
 DB 40 ATGGAACAAAGAAATGTTCTGCTCGGCGCTCTGTGCAATCCGAGTGGGTCTGTACGC 99  
 QY 21 AlaHisCysPheGlnAsnSerTrpThrIleGlyLeuGlyLeuHisSerLeuGluAlaAsp 40  
 DB 100 GACACTGTTTCCAAACTCTTACACCATCGGGCTGGGCTCCACAGTCTTAGGCCGAC 159  
 QY 41 GlnGluProGlySerGlnMetValGluAlaSerLeuSerValArgHisProGluTrpAsn 60  
 DB 160 CAAGAGCCAGGAGCCAGATGGTGGAGGCCAGCTCTCCGTACGGCACCAGACATCAAC 219  
 QY 61 ArgProLeuLeuAlaAsnAspLeuMetLeuIleValLeuAspGluSerValSerGluSer 80  
 DB 220 AGACCCCTTCCTCGCTACACCTCATGCTCATCAAGTTGAGCAATCCCTGTCGGAGTCT 279  
 QY 81 AspThrIleArgSerIleSerIleAlaSerGlnCysProThrAlaGlyAsnSerCysLeu 100  
 DB 280 GACACCATCCGAGCATCGACTGCTGTCAGTCCCTACCGCGGGGAACTCTTGCTTC 339  
 QY 101 ValSerGlyTrpGlyLeuLeuAlaAsnGlyGluLeuThrGlyValCysLeuProSerSer 120  
 DB 340 GTTTCGCTGCGGCTGCTGCTGCGAAGCGTGAAGTCAACGGGTGTGTCTGCTCTTCA 399  
 QY 121 ArgArgSerSerAlaGlnSerArgGlyLeuThrGlnSerSerAlaSerGlnAlaGluCys 140  
 DB 400 AGAGAGTCTCTGCTGCCAGTCCGCGGGGCTGACCCAGAGCTGCTGCCAGCAGCAATGC 459  
 QY 141 LeuProCysCysSerAla 146  
 DB 460 CTACCGTCTGCTGAGTCCG 477

Search completed: August 28, 2006, 18:23:29  
 Job time : 527 secs

Alignment Scores: 8.29e-70 Length: 1265  
 Pred. No.: